

Remarks

Reconsideration of this Application is respectfully requested.

Upon entry of the foregoing amendment, claims 1, 5-13, 18 and 20-29 are pending in the application, with claim 1 being the independent claim. Claims 2-4, 14-17, and 19 are sought to be cancelled without prejudice to or disclaimer of the subject matter therein. New claims 20-29 are sought to be added. Claim 1 has been amended to be directed to Applicants' elected peptides and to clarify the claimed invention. New claims 20-29 depend from claim 1 and are each directed to one of Applicants' elected peptides. Support for claim 1 and new claims 20-29 can be found, *inter alia*, at ¶ 41 and Tables 11-18. Claims 5-9 have been amended to clarify the claimed invention. Support for amended claims 5 and 6 can be found, *inter alia*, at ¶ 69. Support for amended claims 7 and 9 can be found, *inter alia*, at ¶ 98. Support for amended claim 8 can be found, *inter alia*, at ¶ 73. Claim 13 has been amended to be directed to Applicants' elected antigen. These changes are believed to introduce no new matter, and their entry is respectfully requested.

Based on the above amendment and the following remarks, Applicants respectfully request that the Examiner reconsider all outstanding objections and rejections and that they be withdrawn.

Objection to the Oath/Declaration

The Examiner has objected to the Oath/Declaration of April 5, 2005, citing that non-initialed and/or non-dated alterations have been made to the oath or declaration. (Office Action, ¶ 6, Page 3.) Applicants note that the Declaration submitted to the U.S.

Receiving Office upon filing of the corresponding International Application did not contain any such alterations. Applicants are resubmitting herewith a copy of the Declaration as originally submitted.

It appears that the alterations in the scanned version of the Declaration on the PAIR system were made to the document by USPTO personnel subsequent to the submission of the Declaration by Applicants. Applications respectfully request that the Examiner consider the resubmitted Declaration, which does not contain any alterations, and withdraw the outstanding objection.

Objection to the Abstract

The Examiner has objected to the abstract of the disclosure. (Office Action, ¶ 8, Page 3.) Applicants have amended herewith the abstract of the disclosure. Accordingly, Applicants respectfully request that the Examiner reconsider and withdraw the outstanding objection.

Objections to the Specification

The Examiner has objected to the specification because it does not provide sequence identifiers for the peptide sequences of \geq four (4) amino acid residues in length pursuant to 37 C.F.R. § 1.821 (c) and/or (d), for example, in Tables 5, 6, and 11-29. (Office Action, ¶ 9, Page 3.)

Applicants have submitted herewith replacement pages for Tables 11-29 that include sequence identifiers as required by 37 C.F.R. §§ 1.821 (c) and/or (d).

Applicants have also submitted herewith replacement pages for Tables 5 and 6. Applicants note that the amino acids listed in Tables 5 and 6 refer to amino acids that can be present in the alternative at certain anchor residue positions (p1=position 1; p4=position 4; and p6=position 6) of an HLA-DR core motif for the HLA alleles DR supertype, DR3a or DR3b. The amino acids are referred to by their standard single letter designations. As an example, for the DR3 supertype, the anchor residues at position (p1) can be, in the alternative, a leucine (L), an isoleucine (I), a valine (V), a methionine (M), a phenylalanine (F), a tryptophan (W), or a tyrosine(Y). All of the amino acids listed in Tables 5 and 6 are alternative amino acids at the positions indicated according to the designation described above.

In order to clarify that these amino acids are present in the alternative at the positions indicated, Applicants have amended Tables 5 and 6 to include a comma between each amino acid. Because the amino acids in Tables 5 and 6 correspond to individual amino acids, they are not peptide sequences of ≥ 4 amino acid residues in length, and thus no corresponding sequence identifier is required pursuant to 37 C.F.R. §§ 1.821 (c) and/or (d).

The Examiner has further objected to the legend of Figure 1 because it does not recite the sequence identifiers for the anchor residues having \geq four (4) amino acid residues shown in Figure 1. (Office Action, ¶ 10, Page 3.) Applicants note that the amino acids shown in Figure 1, similar to those shown in Tables 5 and 6, refer to amino acids that can be present in the alternative at the designated anchor residue positions, and thus refer to single amino acids, rather than a peptide sequence having \geq four (4) amino

acid residues. Applicants have amended the figure legend to Figure 1 herewith to clarify this.

Accordingly, based on the above amendments to the specification, Applicants respectfully request that the Examiner reconsider and withdraw the outstanding objections.

Rejections under 35 U.S.C. § 112, second paragraph

Claims 1, 3-15 and 18 have been rejected under 35 U.S.C. § 112, second paragraph, as allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regard as their invention. (Office Action, ¶ 11, Page 3.)

The Examiner has alleged that claims 1, 3-15 and 18 are indefinite for reciting "peptides" because in claim 1 it is not clear what the metes and bounds of the size of the peptide is. (Office Action, ¶ 11a, Page 3.) Without acquiescing to the Examiner's rejection and solely in efforts to expedite prosecution, Applicants have amended claim 1 to clarify the claimed invention. Applicants assert that the claims as amended are clear as to the invention's metes and bounds.

The Examiner has also alleged that in claims 3 and 5, the phrase "HTL epitope" is not defined by the claims or in the specification, and it is not clear what the metes and bounds of the phrase are with respect to the overall composition. (Office Action, ¶ 11b, Page 3.) Without acquiescing to the Examiner's rejection and solely in efforts to expedite prosecution, Applicants note that claim 3 has been cancelled. Applicants also assert that the phrase "HTL epitope" is clear from the specification. The specification

discloses that HTL refers to "helper T lymphocyte" and describes peptide fragments that activate such helper T lymphocytes:

MHC molecules are classified as either class I or class II. Class II MHC molecules are expressed primarily on activated lymphocytes and antigen-presenting cells. CD4+ T lymphocytes are activated with recognition of a unique peptide fragment presented by a class II MHC molecule, usually found on an antigen presenting cell like a macrophage or dendritic cell. Often known as *helper T lymphocytes (HTL)*, CD4+ lymphocytes proliferate and secrete cytokines that either support a antibody-mediated response through the production of IL-4 and IL-10 or support a cell-mediated response through the production of IL-2 and IFN- γ .

(Specification, ¶ 2 (emphasis added).) The specification further describes that the unique peptide fragment presented by a class II MHC molecule is an "epitope" of the native antigen:

The MHC-binding peptides identified herein represent epitopes of a native antigen. With regard to a particular amino acid sequence, an epitope is a set of amino acid residues which is recognized by a particular antibody or T cell receptor. Such epitopes are usually presented to lymphocytes via the MHC-peptide complex. An epitope retains the collective features of a molecule, such as primary, secondary and tertiary peptide structure, and charge, that together form a site recognized by an antibody, T cell receptor or MHC molecule.

(Specification, ¶ 35.) In addition, the specification describes that "[o]ne embodiment of an HTL-inducing peptide is less than 50 residues in length and usually consist of between about 6 and about 30 residues, more usually between about 12 and 25, and often between about 15 and 20 residues, for example 15, 16, 17, 18, 19, or 20 residues."

(Specification, ¶ 41.) Specific examples, of such HTL-inducing peptides are disclosed, for example, in Tables 23-27. Thus, as shown above, the specification clearly sets forth

what is meant by the phrase "HTL epitope" and discloses specific examples of such HTL epitopes. Without acquiescing to the Examiners rejection and solely in efforts to expedite prosecution, Applicants have amended claim 5 to clarify the metes and bounds of the phrase with respect to the overall composition.

The Examiner has further alleged that claims 3-5 and 8 are indefinite because it is not clear how the HTL and CTL epitope and the MHC targeting sequences are related to the peptides of claim 1. (Office Action, ¶ 11c, Page 3.) Without acquiescing to the Examiner's rejection, Applicants have cancelled claims 3 and 4. Applicants note that the limitation of claim 4 has been incorporated into amended claim 1. Applicants have amended claims 5 and 8 to clarify the relationship of the HTL epitope and the MHC targeting sequence to the peptides of claim 1.

The Examiner has further alleged that claims 1, 6, 7 and 9 are indefinite as to how the "spacer molecule" (Claim 6), "carrier: (Claim 7) and "lipid" (Claim 9) relate to the peptides of the composition of claim 1. (Office Action, ¶ 11d, Page 3.) Without acquiescing to the Examiner's rejection, Applicants have amended claims 6, 7, and 9 to clarify the relationship of the spacer molecule, carrier and lipid to the peptides of claim 1.

The Examiner has also alleged that claims 11 and 12 are indefinite because the terms "heteropolymer" and "homopolymer" are not defined in the specification, and it is not clear what the metes and bounds of the terms are with respect to the overall composition. (Office Action, ¶ 11e, Page 3.) The specification states that peptide(s) of the invention may be:

. . . linked to its own carrier or as a homopolymer or heteropolymer of active peptide units. Such a polymer has the advantage of increased immunological reaction and, where different peptides are used to make up the polymer, the additional ability to induce antibodies and/or CTLs that react with different antigenic determinants of the virus or tumor cells.

(Specification, ¶ 98.) Thus, the specification discusses that the units of a homopolymer or heteropolymer are the peptides of the invention. Furthermore, the terms "homo" and "hetero" are clear on their face, and would be clearly understood by one of ordinary skill in the art to mean "same" and "different," respectively. Thus, one of ordinary skill in the art would understand that a "homopolymer" is made up of the same polymer units, and a "heteropolymer" is made up of different polymer units. In view of the specification describing that the units of such polymers are individual peptides of the invention, it can be readily understood from the specification that the meaning of "homopolymer" is a polymer with each unit composed of the same peptide, whereas a "heteropolymer" is a polymer with units composed of different peptides.

In view of the discussion above, Applicants respectfully assert that the pending claims comply with the requirements of 35 U.S.C. § 112, second paragraph. Accordingly, Applicants respectfully request that the Examiner reconsider and withdraw the outstanding rejections.

Rejections under 35 U.S.C. § 112, first paragraph

Claims 3-5, 8, 11 and 12 are rejected under 35 U.S.C. § 112, first paragraph, as allegedly failing to comply with the enablement requirement. (Office Action, ¶ 12, Page 6.) Applicants respectfully disagree and traverse the rejection.

As an initial matter, without acquiescing to the Examiner's rejection and solely in efforts to expedite prosecution, Applicants have cancelled claims 3 and 4. As discussed further below, Applicants assert that claims 5, 8, 11 and 12 are enabled.

The Examiner has alleged that

The specification does not show that any of the elected peptides has any of the claimed functional properties, namely, CTL-induction, HTL-induction or MHC targeting. The specification does not provide a single working example for any one of the elected peptides demonstrating that the peptide has one or more of the claimed functional properties in a relevant bioassay or animal model.

(Office Action, Page 7, ¶ 12.)

"As concerns the breadth of a claim relevant to enablement, the only relevant concern should be whether the scope of enablement provided to one skilled in the art by the disclosure is commensurate with the scope of protection sought by the claims." MPEP § 2164.08 (2006) (citing *AK Steel Corp. v. Sollac*, 344 F.3d 1234, 1244 (Fed. Cir. 2003); *In re Moore*, 439 F.2d 1232, 1236 (C.C.P.A. 1971); *see also Plant Genetic Sys., N.V. v. DeKalb Genetics Corp.*, 315 F.3d 1335, 1339 (Fed. Cir. 2003).

Applicants note that the pending claims, as indicated by the Examiner, are directed to a *composition* comprising one or more peptides selected from the peptides of SEQ ID NOs: 53, 55, 139, 502, 527, 627, 673, 807, 846 and 859. (Office Action, ¶ 12, Page 6, "Nature of the Invention.") Applicants point out that the claims do not require any further limitations. Although the Examiner refers to the "claimed" functional properties of the elected peptides, Applicants again note that the claims are only directed to a composition comprising one or more of the elected peptides and do not recite any further claimed features.

Moreover, as long as the specification discloses at least one method for making and using the claimed invention that bears a reasonable correlation to the entire scope of the claim, then the enablement requirement of 35 U.S.C. § 112 is satisfied. *In re Fisher*, 427 F.2d 833, 839, 166 USPQ 18, 24 (CCPA 1970). Additionally, "a specification disclosure which contains a teaching of the manner and process of making and using the invention must be taken as in compliance with the enabling requirement of the first paragraph of § 112 unless there is reason to doubt the objective truth of the statements contained therein which must be relied upon for enabling support." *Rasmusson v. Smithkline Beecham Corp.*, 413 F.3d 1318, 1323 (Fed. Cir. 2005) (quoting *In re Marzocchi*, 439 F.2d 220, 223 (C.C.P.A. 1971)).

Applicants assert that the specification discloses how to make and use compositions comprising the elected peptides and how to test these compositions for binding affinity using various assays. (Specification, ¶ 55-59.) The specification also discloses how to test these compositions for inhibition of CTL or HTL recognition using purified MHC molecules and radioiodinated peptides and/or cells by immunofluorescent staining and flow microfluorometry, or peptide-dependent class I assembly assays. (Specification, ¶ 77.) The specification also discusses the use of mutant mammalian cell lines to test for the capacity of compositions comprising a particular peptide to induce *in vitro* primary CTL responses. (Specification, ¶ 78.) Additionally, the specification discloses how such compositions can be made. (See Specification, ¶ 61-75.)

Thus, as discussed above, the specification not only discloses how to make and use compositions comprising Applicants' elected peptides, the specification also teaches how to assay the efficacy of such compositions and determine whether the particular

peptides have the capacity to bind to certain MHC molecules and/or have the ability to induce an immune response. Thus, the specification discloses "at least one method for making and using the claimed invention that bears a reasonable correlation to the entire scope of the claim."

The purpose of the requirement that the specification describe the invention in such terms that one skilled in the art can make and use the claimed invention without undue experimentation (*i.e.*, the enablement requirement) is to ensure that the invention is communicated to the interested public in a meaningful way. Here, Applicants respectfully assert that the information contained in the disclosure of the specification is sufficient to inform those skilled in the relevant art how to both make and use the claimed invention in a manner that satisfies the requirements of 35 U.S.C. § 112, first paragraph for enablement.

Finally, the Examiner cites several documents referring to the "inherent risks associated with T-cell immunogenic peptides in general." (Office Action, ¶ 12, Pages 7-9.) The fact that experimentation may be complex does not necessarily make it undue, if the art typically engages in such experimentation. *In re Certain Limited-Charge Cell Culture Microcarriers*, 221 USPQ 1165, 1174 (Int'l Trade Comm'n 1983), *aff'd. sub nom.*, *Massachusetts Institute of Technology v. A.B. Fortia*, 774 F.2d 1104, 227 USPQ 428 (Fed. Cir. 1985). See also *In re Wands*, 858 F.2d at 737, 8 USPQ2d at 1404. Here Applicants respectfully assert that not only is no experimentation necessary to practice the claimed invention, but even if any experimentation was performed it would not be undue as it would be of the type typically engaged in by artisans in this art.

Claims 14 and 15 are rejected under 35 U.S.C. § 112, first paragraph, as allegedly failing to comply with the enablement requirement. (Office Action, ¶ 13, Page 6.) Without acquiescing to the Examiner's rejection and solely in efforts to expedite prosecution, Applicants have cancelled claims 14 and 15. The rejections of these claims has therefore been rendered moot. Accordingly, Applicants respectfully request that the Examiner reconsider and withdraw the outstanding rejection.

Other Matters

Applicants note that the Examiner has indicated that Applicants' elected peptides (SEQ ID NOs: 53, 55, 139, 502, 527, 627, 673, 807, 846 and 859) are free of the prior art.

Conclusion

All of the stated grounds of objection and rejection have been properly traversed, accommodated, or rendered moot. Applicants therefore respectfully request that the Examiner reconsider all presently outstanding objections and rejections and that they be withdrawn. Applicants believe that a full and complete reply has been made to the outstanding Office Action and, as such, the present application is in condition for allowance. If the Examiner believes, for any reason, that personal communication will expedite prosecution of this application, the Examiner is invited to telephone the undersigned at the number provided.

Prompt and favorable consideration of this Amendment and Reply is respectfully requested.

Respectfully submitted,

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.



Mita Mukherjee
Agent for Applicants
Registration No. 54,325

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1100 New York Avenue, N.W.
Washington, D.C. 20005-3934
(202) 371-2600

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usually consists of about 8, 9, 10 or 11 residues, preferably 9 or 10 residues. In one embodiment, HLA-DR3 a binding is characterized by an L, I, V, M, F or Y residue at position 1 and a D or E residue at position 4. In another embodiment, HLA-DR3 b binding is characterized by an L, I, V, M, F, Y or A residue at position 1, a D, E, N, Q, S or T residue at position 4, and a K, R or H residue at position 6. In another embodiment, key anchor residues of a DR supertype binding motif are an L, I, V, M, F, W or Y residue at position 1 and an L, I, V, M, S, T, P, C or A residue at position 6. See table 5.

TABLE 5
HLA-DR motifs

	Anchor residues of HLA-DR core motifs		
	p1	p4	p6
DR supertype	<u>LIVMFYW</u> <u>L,I,V,M,F,W,Y</u>	--	<u>LIVMSTPCA</u> <u>L,I,V,M,S,T,P,C,A</u>
DR3 a	<u>LIVMFY</u> <u>L,I,V,M,F,Y</u>	<u>DE</u> <u>D,E</u>	--
DR3 b	<u>LIVMFYA</u> <u>L,I,V,M,F,Y,A</u>	<u>DENQST</u> <u>D,E,N,Q,S,T</u>	<u>KRH</u> <u>K,R,H</u>

Moreover, in another embodiment, murine Db binding is characterized by an N residue at position 5 and L, I, V or M residue at the C-terminal position. In yet another embodiment, murine Kb binding is characterized by a Y or F residue at position 5 and an L, I, V or M residue at the C-terminal position. In an additional embodiment, murine Kd binding is characterized a Y or F residue at position 2 and an L, I, V, or M residue at the C-terminal position. In a further embodiment, murine Kk binding is characterized by an E or D residue at position 2 and an L, I, M, V, F, W, Y or A residue at the C-terminal position. In a further embodiment, murine Ld binding is characterized by a P residue at position 2 and an L, I, M, V, F, W or Y residue at the C-terminal position. See Table 6.

Table 6
Murine Class I Motifs

Allele	Anchor residues of mouse class I motifs			
	p2	p3	p5	C terminus
Db	--	--	N	<u>LIVML</u> ,I,V,M
Dd	G	P	--	<u>LVIL</u> ,V,I
Kb	--	--	YF	<u>LVIML</u> ,V,I,M
Kd	YF	--	--	<u>LVIML</u> ,V,I,M
Kk	ED	--	--	<u>LIMVAL</u> ,I,M,V,A
Ld	P	--	--	<u>LIMVFWYL</u> ,I,M,V,F,W,Y

The peptides present in the invention can be identified by any suitable method. For example, peptides are conveniently identified using the algorithms of the invention described in the co-pending U.S. Patent Application Serial No. 09/894,018. These algorithms are mathematical procedures that produce a score which enables the selection of immunogenic peptides. Typically one uses the algorithmic score with a binding threshold to enable selection of peptides that have a high probability of binding at a certain affinity and will in turn be immunogenic. The algorithm are based upon either the effects on MHC binding of a particular amino acid at a particular position of a peptide or the effects on binding MHC of a particular substitution in a motif containing peptide.

Peptide sequences characterized in molecular binding assays and capture assays have been and can be identified utilizing various technologies. Motif-positive sequences are identified using a customized application created at Epimmune. Sequences are also identified utilizing matrix-based algorithms, and have been used in conjunction with a "power" module that generates a predicted 50% inhibitory concentration (PIC) value. These latter methods are operational on Epimmune's HTML-based Epitope Information System (EIS) database. All of the described methods are viable options in peptide sequence selection for IC₅₀ determination using binding assays.

Additional procedures useful in identifying the peptides of the present invention generally follow the methods disclosed in Falk *et al.*, *Nature*

TABLE 11

HLA-A1 SUPERTYPE

Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
AYGPGPGKF	<u>1</u>	9	Artificial sequence	Consensus		A
AEIPYLAKY	<u>2</u>	9	Artificial sequence	pool consensus		A
AADAAAAY	<u>3</u>	9	Artificial sequence			PolyA
AYSSWMYSY	<u>4</u>	9	EBV	EBNA3	176	
LAEKTKEY	<u>5</u>	9	FluA	POL2	16	
GTYDYWAGY	<u>6</u>	9	Gonorrhea			
LSVHSIQNDY	<u>7</u>	10	Gonorrhea			
DTGQCPELVY	<u>8</u>	10	Gonorrhea			
DLLDTASALY	<u>9</u>	10	HBV	Core	419	
WFHISCLTF	<u>10</u>	9	HBV	NUC	102	
LSLDVSAAFY	<u>11</u>	10	HBV	pol	426	
LSGPGPGAFY	<u>12</u>	10	HBV	pol	426	A
LSLGPFGFY	<u>13</u>	10	HBV	pol	426	A
LSLDGPGPGY	<u>14</u>	10	HBV	pol	426	A
KTYGRKLHLY	<u>15</u>	10	HBV	pol	1098	
KTGPGPGHLY	<u>16</u>	10	HBV	pol	1098	A
KTYGPGPGLY	<u>17</u>	10	HBV	pol	1098	A
KTYGGPGPGY	<u>18</u>	10	HBV	pol	1098	A
KYTSFPWL	<u>19</u>	8	HBV	pol	745	
FAAPFTQCGY	<u>20</u>	10	HBV	pol	631	
SYQHFRKLLL	<u>21</u>	10	HBV	POL	4	
LYSHPIILGF	<u>22</u>	10	HBV	POL	492	
MSTTDLEAY	<u>23</u>	9	HBV	X	103	
MYVGGPGPGVF	<u>24</u>	11	HCV	E1	275	A
VMGSSYGF	<u>25</u>	8	HCV	NS5	2639	
EVDGVRLHRY	<u>26</u>	10	HCV	NS5	2129	
RTEILDLWVY	<u>27</u>	10	HIV	NEF	182	A
RQDILDLWVY	<u>28</u>	10	HIV	NEF	182	A
RTDILDLWVY	<u>29</u>	10	HIV	NEF	182	A
YTDGPGIRY	<u>30</u>	9	HIV	NEF	207	A
ATELHPEYY	<u>31</u>	9	HIV	NEF	322	A
DLWVYHTQGY	<u>32</u>	11	HIV	NEF	188	A
WVYHTQGY	<u>33</u>	9	HIV	NEF	191	A
FFLKEKGGF	<u>34</u>	9	HIV	NEF	116	A
LYVYHTQGY	<u>35</u>	9	HIV	NEF	190	A
ITKILYQSNPY	<u>36</u>	11	HIV	REV	20	A
KTLYQSNPY	<u>37</u>	9	HIV	REV	22	A
PVDPNLEPY	<u>38</u>	9	HIV	TAT	3	A
STVKHHMY	<u>39</u>	8	HIV	VIF	23	A
LSKISEYRHY	<u>40</u>	10	HPV	E6	70	
ISEYRHYNY	<u>41</u>	9	HPV	E6	73	
RFHNIRGRW	<u>42</u>	9	HPV	E6	131	
RFLSKISEY	<u>43</u>	9	HPV	E6	68	
RFHNISGRW	<u>44</u>	9	HPV	E6	124	

HLA-A1 SUPERTYPE

Sequence	SEQ ID		AA	Organism	Protein	Position	Analog
	NO.						
TLEKLTNTGLY	<u>45</u>		11	HPV	E6	89	
TLGPGPGTGLY	<u>46</u>		11	HPV	E6	89	A
TLEGPGPGGLY	<u>47</u>		11	HPV	E6	89	A
TLEKGP GPGLY	<u>48</u>		11	HPV	E6	89	A
TLEKLGP GPGY	<u>49</u>		11	HPV	E6	89	A
TLEKLTNTGLY	<u>50</u>		11	HPV	E6	89	
TLEKITNTELY	<u>51</u>		11	HPV	E6	89	
PYGVCIMCLRF	<u>52</u>		11	HPV	E6	59	
ITDIILECVY	<u>53</u>		10	HPV	E6	30	A
YSDISEYRHY	<u>54</u>		10	HPV	E6	77	A
LTDIEITCVY	<u>55</u>		10	HPV	E6	25	A
YSDIRELRHY	<u>56</u>		10	HPV	E6	72	A
ELSSALEIPY	<u>57</u>		10	HPV	E6	14	
ETSSALEIPY	<u>58</u>		10	HPV	E6	14	A
ELDSALEIPY	<u>59</u>		10	HPV	E6	14	A
YTKVSEFRWY	<u>60</u>		10	HPV	E6	70	A
YSDVSEFRWY	<u>61</u>		10	HPV	E6	70	A
LTDVSIACVY	<u>62</u>		10	HPV	E6	25	A
FTSRIRELRY	<u>63</u>		10	HPV	E6	71	A
YSDIRELRY	<u>64</u>		10	HPV	E6	72	A
LTDLRLSCVY	<u>65</u>		10	HPV	E6	26	A
FTSKVRKYRY	<u>66</u>		10	HPV	E6	72	A
YSDVRKYRY	<u>67</u>		10	HPV	E6	73	A
FYSKVSEFRF	<u>68</u>		10	HPV	E6	69	A
FYSRIRELRF	<u>69</u>		10	HPV	E6	71	A
PYAVCRVCLF	<u>70</u>		10	HPV	E6	62	A
ITEYRHYN	<u>71</u>		9	HPV	E6	73	A
ISDYRHYN	<u>72</u>		9	HPV	E6	73	A
ITEYRHYQY	<u>73</u>		9	HPV	E6	73	A
ISDYRHYQY	<u>74</u>		9	HPV	E6	73	A
LTDLLIRCY	<u>75</u>		9	HPV	E6	99	A
KTDQRSEVY	<u>76</u>		9	HPV	E6	35	A
AYRDL CIVY	<u>77</u>		9	HPV	E6	53	A
KYYSKISEY	<u>78</u>		9	HPV	E6	75	A
KFYSKISEF	<u>79</u>		9	HPV	E6	75	A
RYHNIRGRW	<u>80</u>		9	HPV	E6	131	A
RFHNIRGRF	<u>81</u>		9	HPV	E6	131	A
AYKDLFVVY	<u>82</u>		9	HPV	E6	48	A
LFVVYRDSF	<u>83</u>		9	HPV	E6	52	A
RYHNIAGHY	<u>84</u>		9	HPV	E6	126	A
RFHNIAGHF	<u>85</u>		9	HPV	E6	126	A
VYGT TLEKF	<u>86</u>		9	HPV	E6	83	A
AYADLTVVY	<u>87</u>		9	HPV	E6	46	A
AFADLTVVF	<u>88</u>		9	HPV	E6	46	A
RYLSKISEY	<u>89</u>		9	HPV	E6	68	A
RYHNISGRW	<u>90</u>		9	HPV	E6	124	A

HLA-A1 SUPERTYPE

Sequence	SEQ ID		AA	Organism	Protein	Position	Analog
	NO.						
AYKDLCIVY	<u>91</u>		9	HPV	E6	48	A
RYHSIAGQY	<u>92</u>		9	HPV	E6	126	A
RFHSIAGQF	<u>93</u>		9	HPV	E6	126	A
KYLFTDLRI	<u>94</u>		9	HPV	E6	44	A
KFLFTDLRF	<u>95</u>		9	HPV	E6	44	A
LYTDLRIVY	<u>96</u>		9	HPV	E6	46	A
LFTDLRIVF	<u>97</u>		9	HPV	E6	46	A
RFLSKISEF	<u>98</u>		9	HPV	E6	68	A
EYRHYQYSF	<u>99</u>		9	HPV	E6	75	A
RYHNIMGRW	<u>100</u>		9	HPV	E6	124	A
RFHNIMGRF	<u>101</u>		9	HPV	E6	124	A
NFACTELKF	<u>102</u>		9	HPV	E6	47	A
PYAVCRVCF	<u>103</u>		9	HPV	E6	62	A
LYYSKVRKY	<u>104</u>		9	HPV	E6	71	A
VYADLRIVY	<u>105</u>		9	HPV	E6	46	A
VFADLRIVF	<u>106</u>		9	HPV	E6	46	A
NYSLYGDTF	<u>107</u>		9	HPV	E6	80	A
RFHNISGRF	<u>108</u>		9	HPV	E6	124	A
FTDLTIVY	<u>109</u>		8	HPV	E6	47	
FTDLRIVY	<u>110</u>		8	HPV	E6	47	
TLEKLTNTGLY	<u>111</u>		11	HPV	E6	89	
LTDIEITCVY	<u>112</u>		10	HPV	E6	25	A
LTDVSIACVY	<u>113</u>		10	HPV	E6	25	A
ITDIILECVY	<u>114</u>		10	HPV	E6	30	
KTDQRSEVY	<u>115</u>		9	HPV	E6	35	
FTDLTIVY	<u>116</u>		8	HPV	E6	47	
YSDIRELRY	<u>117</u>		10	HPV	E6	72	A
YTKVSEFRWY	<u>118</u>		10	HPV	E6	70	A
FTSRIRELRY	<u>119</u>		10	HPV	E6	71	A
FTSKVRKYRY	<u>120</u>		10	HPV	E6	72	A
ISDYRHYN	<u>121</u>		9	HPV	E6	73	A
ISEYRHYQY	<u>122</u>		9	HPV	E6	73	
ISDYRHYQY	<u>123</u>		9	HPV	E6	73	A
EYRHYCYSLY	<u>124</u>		10	HPV	E6	82	
EYRHYNYSLY	<u>125</u>		10	HPV	E6	75	
LTDLLIRCY	<u>126</u>		9	HPV	E6	99	
ETRHYCYSLY	<u>127</u>		10	HPV	E6	82	A
EYDHYCYSLY	<u>128</u>		10	HPV	E6	82	A
KTRYDYDSVY	<u>129</u>		10	HPV	E6	78	A
KYDYDYDSVY	<u>130</u>		10	HPV	E6	78	A
ETRHYNYSLY	<u>131</u>		10	HPV	E6	75	A
EYDHYNYSLY	<u>132</u>		10	HPV	E6	75	A
PTLKEYVLDLY	<u>133</u>		11	HPV	E7	6	
HTDTPTLHEY	<u>134</u>		10	HPV	E7	2	A
RTETPTLQDY	<u>135</u>		10	HPV	E7	2	A
ETDPVDLLCY	<u>136</u>		10	HPV	E7	20	A

HLA-A1 SUPERTYPE

Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
QTEQATSNYY	<u>137</u>	10	HPV	E7	46	A
ATDNYYIVTY	<u>138</u>	10	HPV	E7	50	A
LTEYVLDLY	<u>139</u>	9	HPV	E7	8	A
QTEQATSNY	<u>140</u>	9	HPV	E7	46	A
RQAKQHTCY	<u>141</u>	9	HPV	E7	51	
RTAKQHTCY	<u>142</u>	9	HPV	E7	51	A
HTDTPTLHEY	<u>143</u>	10	HPV	E7	2	A
RTETPTLQDY	<u>144</u>	10	HPV	E7	2	A
PTLKEYVLDLY	<u>145</u>	11	HPV	E7	6	
LTEYVLDLY	<u>146</u>	9	HPV	E7	8	A
QAEQATSNY	<u>147</u>	9	HPV	E7	46	
ATSNYYIVTY	<u>148</u>	10	HPV	E7	50	
ATDNYYIVTY	<u>149</u>	10	HPV	E7	50	A
RVLPPNWKY	<u>150</u>	9	Human	40s riboprot S13	132	
RLAHEVGWKY	<u>151</u>	10	Human	60s ribo prot L13A	139	
AYKKQFSQY	<u>152</u>	9	Human	60s ribo prot L5	217	
AADNPPAQY	<u>153</u>	9	Human	CEA	261	A
RSGPGPGNVLY	<u>154</u>	11	Human	CEA	225	A
RSDGPGPGVLY	<u>155</u>	11	Human	CEA	225	A
RSDSGPGPGLY	<u>156</u>	11	Human	CEA	225	A
RSDSVGPGPGY	<u>157</u>	11	Human	CEA	225	A
SLFVSNHAY	<u>158</u>	9	Human	fructose biphosphatealdolase	355	
RWGLLLALL	<u>159</u>	9	Human	Her2/neu	8	
YTGPGPGVY	<u>160</u>	9	Human	Jchain	102	A
YTAGPGPGY	<u>161</u>	9	Human	Jchain	102	A
TQDLVQEKY	<u>162</u>	9	Human	MAGE1	240	
TQGPMPGKY	<u>163</u>	9	Human	MAGE1	240	A
TQDGPMPGY	<u>164</u>	9	Human	MAGE1	240	A
EVGPMPGLY	<u>165</u>	9	Human	MAGE3	161	A
EVDGPMPGY	<u>166</u>	9	Human	MAGE3	161	A
IYGPMPGLIF	<u>167</u>	10	Human	MAGE3	195	A
RISGVDRYY	<u>168</u>	9	Human	NADH ubiquinolreductase	53	
IMVLSFLF	<u>169</u>	8	Pf	CSP	427	
ALFQEYQCY	<u>170</u>	9	Pf	CSP	18	
LSEYYDXDIY	<u>171</u>	10	Pf		347	
FQAAESNERY	<u>172</u>	10	Pf		13	
ELEASISGKY	<u>173</u>	10	Pf		81	
FVSSIFISFY	<u>174</u>	10	Pf		255	
KVSDEIWNYY	<u>175</u>	9	Pf		182	
IMNHLMTLY	<u>176</u>	9	Pf		38	
LIENELMNY	<u>177</u>	9	Pf		149	
NVDQQNDMY	<u>178</u>	9	Pf		182	
SSFFMNRFY	<u>179</u>	9	Pf		309	
QAAESNERY	<u>180</u>	9	Pf		14	

HLA-A1 SUPERTYPE

Sequence	SEQ ID		AA	Organism	Protein	Position	Analog
	NO.						
LEASISGKY	<u>181</u>		9	Pf		82	
NLALLYGEY	<u>182</u>		9	Pf		188	
SSPLFNNFY	<u>183</u>		9	Pf		14	
QNADKNFLY	<u>184</u>		9	Pf		145	
VSSIFISFY	<u>185</u>		9	Pf		256	
SYKSSKRDKF	<u>186</u>		10	Pf		225	
RYQDPQNYEL	<u>187</u>		10	Pf		21	
DFFLKSKFNI	<u>188</u>		10	Pf		3	
NYMKIMNHL	<u>189</u>		9	Pf		34	
TYKKKNNHI	<u>190</u>		9	Pf		264	
SFFMNRFYI	<u>191</u>		9	Pf		310	
FYITTRYKY	<u>192</u>		9	Pf		316	
KYINFINFI	<u>193</u>		9	Pf		328	
TWKPTIFLL	<u>194</u>		9	Pf		135	
KYNYFIHFF	<u>195</u>		9	Pf		216	
HFFTWTGTMF	<u>196</u>		9	Pf		222	
RMTSLKNEL	<u>197</u>		9	Pf		61	
YYNNFNNNY	<u>198</u>		9	Pf		77	
GTDEXRNXY	<u>199</u>		9	Unknown	Naturally processed		A
ETDXXXDRSEY	<u>200</u>		11	Unknown	Naturally processed		A
FTDVNSXXRY	<u>201</u>		10	Unknown	Naturally processed		A
VXDPYNXKY	<u>202</u>		9	Unknown	Naturally processed		A
VADKVHXYMY	<u>203</u>		9	Unknown	Naturally processed		A
ETXXPDWSY	<u>204</u>		9	Unknown	Naturally processed		A
XTHNXVDXY	<u>205</u>		9	Unknown	Naturally processed		A

TABLE 12

HLA-A1 SUPERTYPE

Sequence	SEQ ID		A*0101	A*2902	A*3002
	NO.				
AYGPGPGKF	<u>1</u>			44854	3.2
AEIPYLAKY	<u>2</u>				144
AADAAAAKY	<u>3</u>	20			
AYSSWMYSY	<u>4</u>				4.9
LAECTMKEY	<u>5</u>	174			
GTYDYWAGY	<u>6</u>	141			
LSVHSIQNDY	<u>7</u>	279			
DTGQCPELVY	<u>8</u>	129			
DLLDTASALY	<u>9</u>			74	37
WFHISCLTF	<u>10</u>	85324	95		75094
LSLDVSAAFY	<u>11</u>	267	12		7.1
LSGPGPGAFY	<u>12</u>	25	1383		6.6
LSLGPGPFGY	<u>13</u>	21	132		8.2
LSLDGPGPGY	<u>14</u>	266	274		181
KTYGRKLHLY	<u>15</u>	171	27		1.5
KTGPGPGHLY	<u>16</u>	29	192		1.3
KTYGPGPGLY	<u>17</u>	5.7	227		0.96
KTYGGPGPGY	<u>18</u>	282	228		1.7
KYTSFPWL	<u>19</u>		>172413		346
FAAPFTQCGY	<u>20</u>		461		1364
SYQHFRKLLL	<u>21</u>	>83333	28		3768
LYSHPIILGF	<u>22</u>	3166	109		1116
MSTTDLEAY	<u>23</u>		2565		396
MYVGPGPGVF	<u>24</u>		89		2870
VMGSSYGF	<u>25</u>		145		41967
EVDGVRLHRY	<u>26</u>		14940		113
RTEILDWVY	<u>27</u>	99	10204		315
RQDILDWVY	<u>28</u>	8995	13928		95
RTDILDWVY	<u>29</u>	85	13424		360
YTDGPGIRY	<u>30</u>	11	562		7911
ATELHPEYY	<u>31</u>	43	6608		1734
DLWVYHTQGY	<u>32</u>	5880	852		16
WVYHTQGY	<u>33</u>	703	215		5.6
FFLKEKGGF	<u>34</u>		3015		141
LYVYHTQGY	<u>35</u>		216		258
ITKILYQSNPY	<u>36</u>	>10060	64908		298
KTLYQSNPY	<u>37</u>	6912	1703		35
PVDPNLEPY	<u>38</u>	195	13193		7121
STVKHHMY	<u>39</u>	8132	1760		68
LSKISEYRHY	<u>40</u>	14306	55190		186
ISEYRHYNY	<u>41</u>	25	1329		32
RFHNIRGRW	<u>42</u>	52917	18		58
RFLSKISEY	<u>43</u>	>40322	34623		23
RFHNISGRW	<u>44</u>	48564	174		37

HLA-A1 SUPERTYPE

Sequence	SEQ ID	A*0101	A*2902	A*3002
	NO.			
TLEKLTNTGLY	<u>45</u>	23	991	92
TLGPGPGTGLY	<u>46</u>	350	1320	7.4
TLEGPGPGGLY	<u>47</u>	11	2320	40
TLEKGP GPGLY	<u>48</u>	13	2036	40
TLEKLGP GPGY	<u>49</u>	269	4473	1962
TLEKLTNTGLY	<u>50</u>	77	5500	154
TLEKITNTELY	<u>51</u>	17	8402	3897
PYGV CIMCLRF	<u>52</u>		69	43722
ITDIILECVY	<u>53</u>	1.8	7660	505
YSDISEYRHY	<u>54</u>	3.8	1350	514
LTDIEITCVY	<u>55</u>	12	540	80
YSDIRELRHY	<u>56</u>	14	1137	740
ELSSALEIPY	<u>57</u>	171	6031	4472
ETSSALEIPY	<u>58</u>	19	12026	7144
ELDSALEIPY	<u>59</u>	38	82189	38284
YTKVSEFRWY	<u>60</u>	276	3308	420
YSDVSEFRWY	<u>61</u>	3.9	1842	1026
LTDVSIACVY	<u>62</u>	2.9	764	72
FTSRIRELRY	<u>63</u>	4.4	77	50
YSDIRELRY	<u>64</u>	9.4	733	456
LTDLRLSCVY	<u>65</u>	45	1783	613
FTSKVRKYRY	<u>66</u>	64	6677	52
YSDVRKYRY	<u>67</u>	19	849	794
FYSKVSEFRF	<u>68</u>		79	18453
FYSRIRELRF	<u>69</u>		83	12598
PYAVCRVCLF	<u>70</u>		407	5226
ITEYRHYN	<u>71</u>	114	625	418
ISDYRHYN	<u>72</u>	16	45	455
ITEYRHYQY	<u>73</u>	90	1030	526
ISDYRHYQY	<u>74</u>	13	37	382
LTDLLIRCY	<u>75</u>	13	6857	5515
KTDQRSEVY	<u>76</u>	84	200429	1174
AYRDL CIVY	<u>77</u>		7117	66
KYYSKISEY	<u>78</u>		702	1.3
KFY SKISEF	<u>79</u>		73339	306
RYHNIRGRW	<u>80</u>		122644	15
RFHNIRGRF	<u>81</u>		346	0.69
AYKDLFVVY	<u>82</u>		639	1.3
LFVVYRDSF	<u>83</u>		919	18
RYHNIAGHY	<u>84</u>		138	0.93
RFHNIAGHF	<u>85</u>		635	1.4
VYGT TLEKF	<u>86</u>		75267	220
AYADLT VVY	<u>87</u>		136	9.3
AFADLT VVF	<u>88</u>		779	137
RYLSKISEY	<u>89</u>		4247	1.1
RYHNISGRW	<u>90</u>		104884	13

HLA-A1 SUPERTYPE

Sequence	SEQ ID		A*0101	A*2902	A*3002
	NO.				
AYKDLICIVY	<u>91</u>			5205	29
RYHSLAGQY	<u>92</u>			544	1.4
RFHSIAGQF	<u>93</u>			481	1.2
KYLFTDLRI	<u>94</u>			78575	339
KFLFTDLRF	<u>95</u>			44	152
LYTDLRIVY	<u>96</u>			4.8	2.1
LFTDLRIVF	<u>97</u>			164	2649
RFLSKISEF	<u>98</u>			40103	201
EYRHYQYSF	<u>99</u>			13707	430
RYHNIMGRW	<u>100</u>			106990	7.1
RFHNIMGRF	<u>101</u>			174	1.3
NFACTELKF	<u>102</u>			46	6826
PYAVCRVCF	<u>103</u>			5602	316
LYYSKVRKY	<u>104</u>			1452	28
VYADLRIVY	<u>105</u>			8.2	8.3
VFADLRIVF	<u>106</u>			87	24062
NYSLYGDTF	<u>107</u>			20945	64
RFHNISGRF	<u>108</u>			572	2.8
FTDLTIVY	<u>109</u>	16		1275	39043
FTDLRIVY	<u>110</u>	26		813	8060
TLEKLTNTGLY	<u>111</u>	174			
LTDIEITCVY	<u>112</u>	33			
LTDVSIACVY	<u>113</u>	57			
ITDIILECVY	<u>114</u>	187			
KTDQRSEVY	<u>115</u>	41			
FTDLTIVY	<u>116</u>	34			
YSDIRELRY	<u>117</u>	20			
YTKVSEFRWY	<u>118</u>	204			
FTSRIRELRY	<u>119</u>	25			
FTSKVRKYRY	<u>120</u>	37			
ISDYRHYN	<u>121</u>	28			
ISEYRHYQY	<u>122</u>	40			
ISDYRHYQY	<u>123</u>	28			
EYRHYCYSLY	<u>124</u>	125		198	3.7
EYRHYNYSLY	<u>125</u>	111027		956	12
LTDLLIRCY	<u>126</u>	64			
ETRHYCYSLY	<u>127</u>	43		755	10
EYDHYCYSLY	<u>128</u>	110081		799	77
KTRYDYSVY	<u>129</u>	2957		87841	0.71
KYDYYDYSVY	<u>130</u>	186339		5749	11
ETRHYNYSLY	<u>131</u>	445		5464	29
EYDHYNYSLY	<u>132</u>	11251		777	93
PTLKEYVLDLY	<u>133</u>	195		805	408
HTDTPTLHEY	<u>134</u>	20		1509	54
RTETPTLQDY	<u>135</u>	11		1987	239
ETDPVDLLCY	<u>136</u>	6.4		4110	52640

HLA-A1 SUPERTYPE

Sequence	SEQ ID		A*0101	A*2902	A*3002
	NO.				
QTEQATSNYY	<u>137</u>	11		9576	500
ATDNYYIVTY	<u>138</u>	7.4		1918	65
LTEYVLDLY	<u>139</u>	6.0		941	81
QTEQATSNY	<u>140</u>	14		119081	3247
RQAKQHCTY	<u>141</u>	>135135		155246	108
RTAKQHCTY	<u>142</u>	5647		130343	346
HTDTPTLHEY	<u>143</u>	30			
RTETPTLQDY	<u>144</u>	40			
PTLKEYVLDLY	<u>145</u>	426			
LTEYVLDLY	<u>146</u>	8.0			
QAEQATSNY	<u>147</u>	132			
ATSNNYIVTY	<u>148</u>	428			
ATDNYYIVTY	<u>149</u>	19			
RVLPPNWKY	<u>150</u>				3.0
RLAHEVGWKY	<u>151</u>				3.8
AYKKQFSQY	<u>152</u>				5.3
AADNPPAQY	<u>153</u>	9.2			
RSGPGPGNVLY	<u>154</u>	172		11270	6.3
RSDGPGPGVLY	<u>155</u>	12		13162	12
RSDSGPGPGLY	<u>156</u>	3.3		11856	4.2
RSDSVGPGPGY	<u>157</u>	23		31193	33
SLFVSNHAY	<u>158</u>				1.1
RWGLLLALL	<u>159</u>			61253	300
YTGPGPVY	<u>160</u>	2.7		2015	6.4
YTAGPGPGY	<u>161</u>	7.0		28	755
TQDLVQEKY	<u>162</u>	57		33304	3796
TQGPGPVKY	<u>163</u>	4192		36746	3.2
TQDGPGPY	<u>164</u>	381		37093	541
EVGPGPGLY	<u>165</u>	50		18183	45
EVDGPGPY	<u>166</u>	29		25775	5766
IYGPGPGLIF	<u>167</u>			58	6845
RISGVDRYY	<u>168</u>				3.0
IMVLSFLF	<u>169</u>			111	30000
ALFQEYQCY	<u>170</u>	>42016		149	1032
LSEYYDXDIY	<u>171</u>	11		1647	489
FQAAESNERY	<u>172</u>	8958		1780	372
ELEASISGKY	<u>173</u>	142		21934	463
FVSSIFISFY	<u>174</u>	118		22	84
KVSDEIWNYY	<u>175</u>	435		230	1.9
IMNHLMTLY	<u>176</u>	150		1.7	1.8
LIENELMNY	<u>177</u>	412		3936	169
NVDQQNDMY	<u>178</u>	47		22173	79057
SSFFMNRFY	<u>179</u>	239		36	7.5
QAAESNERY	<u>180</u>	353		24281	3011
LEASISGKY	<u>181</u>	57792		17824	87
NLALLYGEY	<u>182</u>	275		138	102

HLA-A1 SUPERTYPE

Sequence	SEQ ID		A*0101	A*2902	A*3002
	NO.				
SSPLFNIFY	<u>183</u>		117	389	73
QNADKNFLY	<u>184</u>		3811	24	663
VSSIFISFY	<u>185</u>		144	1800	55
SYKSSKRDKF	<u>186</u>			12594	88
RYQDPQNYEL	<u>187</u>			79717	189
DFFLKSKFNI	<u>188</u>			47714	491
NYMKIMNHL	<u>189</u>			45443	110
TYKKKNNHI	<u>190</u>			21642	162
SFFMNRFYI	<u>191</u>			200	1022
FYITTRYKY	<u>192</u>			9.6	7.5
KYINFINFI	<u>193</u>			25475	55
TWKPTIFLL	<u>194</u>			21155	306
KYNYFIHFF	<u>195</u>			319	2.7
HFFTWGTMF	<u>196</u>			4.0	220
RMTSLKNEL	<u>197</u>			40270	14
YYNNFNNNY	<u>198</u>			19	34
GTDEXRNXY	<u>199</u>	0.67			
ETDXXXDRSEY	<u>200</u>	2.0			
FTDVNSXXRY	<u>201</u>	0.20			
VXDPYNXKY	<u>202</u>	2.3			
VADKVHXY	<u>203</u>	2.4			
ETXXPDWSY	<u>204</u>	11			
XTHNXVDXY	<u>205</u>	1.4			

TABLE 13

HLA-A2 SUPERTYPE

Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
PPFKYAAAV	<u>206</u>	9	Artificial sequence			A
AMAKAAAV	<u>207</u>	9	Artificial sequence			PolyA
AMAKAAAL	<u>208</u>	9	Artificial sequence			PolyA
AMAKAAAT	<u>209</u>	9	Artificial sequence			PolyA
AXAKAAAL	<u>210</u>	9	Artificial sequence			PolyA
FVYGGSKTSL	<u>211</u>	10	EBNA		508	
ILGPGPGL	<u>212</u>	8	Flu	M1	59	A
GILGFVFTL	<u>213</u>	9	Flu	M1	58	
GLIYNRMGAV	<u>214</u>	10	Flu A	M1	129	
VLMEWLKTRPI	<u>215</u>	11	Flu A	M1	41	
FLPSDYFPSV	<u>216</u>	10	HBV	Core	18	A
FLGPGGPSV	<u>217</u>	10	HBV	core	18	A
FLPGPGPSV	<u>218</u>	10	HBV	core	18	A
FLPSGPGPGV	<u>219</u>	10	HBV	core	18	A
WLGPGPGFV	<u>220</u>	9	HBV	env	335	A
WLSGPGPGV	<u>221</u>	9	HBV	env	335	A
GVLGWSPQV	<u>222</u>	9	HBV	env	62	A
PVLPIFFCV	<u>223</u>	9	HBV	env	377	A
VVQAGFFLV	<u>224</u>	9	HBV	env	177	A
FLLAQFTSAI	<u>225</u>	10	HBV	Pol	503	
YLLTLWKAGI	<u>226</u>	10	HBV	pol	147	
YLGPGPGAGI	<u>227</u>	10	HBV	pol	147	A
YLLGPGPGGI	<u>228</u>	10	HBV	pol	147	A
YLLTGPGPGI	<u>229</u>	10	HBV	pol	147	A
HVYSHPIIV	<u>230</u>	9	HBV	pol	1076	A
FVLSLGIHV	<u>231</u>	9	HBV	pol	562	A
YVDDVVLGV	<u>232</u>	9	HBV	pol	538	A
IVRGTSFVYV	<u>233</u>	10	HBV	pol	773	A
SLGPGPGIAV	<u>234</u>	10	HIV	env	814	A
SLLGPGPGAV	<u>235</u>	10	HIV	env	814	A
SLLNGPGPGV	<u>236</u>	10	HIV	env	814	A
KITPLCVTL	<u>237</u>	9	HIV	Env	134	A
KLTPLCVTM	<u>238</u>	9	HIV	Env	134	A
KLTPLCVPL	<u>239</u>	9	HIV	Env	134	A
KLTPLCVSL	<u>240</u>	9	HIV	Env	134	A
KLTPLCITL	<u>241</u>	9	HIV	Env	134	A
QLTPLCVTL	<u>242</u>	9	HIV	Env	134	A
KLTPRCVTL	<u>243</u>	9	HIV	Env	134	A
ELTPLCVTL	<u>244</u>	9	HIV	Env	134	A
QMTFLCVQM	<u>245</u>	9	HIV	Env	134	A
KMTFLCVQM	<u>246</u>	9	HIV	Env	134	A
KLTPLCVAL	<u>247</u>	9	HIV	Env	134	A
KLTPFCVTL	<u>248</u>	9	HIV	Env	134	A
SLYNTVATL	<u>249</u>	9	HIV	GAG	77	
VLAEAMSQT	<u>250</u>	9	HIV	Gag	386	A
VLAEAMSQA	<u>251</u>	9	HIV	Gag	386	A

HLA-A2 SUPERTYPE

Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
VLAEAMSQI	<u>252</u>	9	HIV	Gag	386	A
ILAEAMSQV	<u>253</u>	9	HIV	Gag	386	A
VLAEAMSKV	<u>254</u>	9	HIV	Gag	386	A
VLAEAMSHA	<u>255</u>	9	HIV	Gag	386	A
ILAEAMSQA	<u>256</u>	9	HIV	Gag	386	A
VLAEAMSRA	<u>257</u>	9	HIV	Gag	386	A
VLAEAMATA	<u>258</u>	9	HIV	Gag	386	A
ILAEAMASA	<u>259</u>	9	HIV	Gag	386	A
MTHNPPIPV	<u>260</u>	9	HIV	Gag	271	A
MTNPPVPV	<u>261</u>	9	HIV	Gag	271	A
MTSNPPIPV	<u>262</u>	9	HIV	Gag	271	A
MTSNPPVPV	<u>263</u>	9	HIV	Gag	271	A
MTSDPPIPV	<u>264</u>	9	HIV	Gag	271	A
MTGNPPIPV	<u>265</u>	9	HIV	Gag	271	A
MTGNPPVPV	<u>266</u>	9	HIV	Gag	271	A
MTGNPAIPV	<u>267</u>	9	HIV	Gag	271	A
MTGNPSIPV	<u>268</u>	9	HIV	Gag	271	A
MTANPPVPV	<u>269</u>	9	HIV	Gag	271	A
SLYNTVATL	<u>270</u>	9	hiv	gag	77	
QAHCNISRA	<u>271</u>	9	HIV	gp160	332	
FLKEKGGV	<u>272</u>	8	HIV	NEF	117	A
GLGAVSRDL	<u>273</u>	9	HIV	NEF	45	A
GLITSSNTA	<u>274</u>	9	HIV	NEF	62	A
ALEEEVGFPV	<u>275</u>	11	HIV	NEF	83	A
FLKEKGGLEGV	<u>276</u>	11	HIV	NEF	117	A
FLKEKGGLDGV	<u>277</u>	11	HIV	NEF	117	A
GLIYSKKRQEV	<u>278</u>	11	HIV	NEF	173	A
LLYSKKRQEI	<u>279</u>	10	HIV	NEF	174	A
LLYSKKRQEIL	<u>280</u>	11	HIV	NEF	174	A
RLDILDLWV	<u>281</u>	9	HIV	NEF	182	A
EILDLWVYHV	<u>282</u>	10	HIV	NEF	185	A
ILDLWVYHV	<u>283</u>	9	HIV	NEF	186	A
ILDLWVYNV	<u>284</u>	9	HIV	NEF	186	A
WLNYTPGPGT	<u>285</u>	10	HIV	NEF	204	A
WQNYTPGPGV	<u>286</u>	10	HIV	NEF	204	A
WLNYTPGPGI	<u>287</u>	10	HIV	NEF	204	A
YLPGPGIRYPL	<u>288</u>	11	HIV	NEF	207	A
YTPGPGIRYPV	<u>289</u>	11	HIV	NEF	207	A
LLFGWCFLK	<u>290</u>	9	HIV	NEF	221	A
LTFGWCFKV	<u>291</u>	9	HIV	NEF	221	A
LLFGWCFLV	<u>292</u>	10	HIV	NEF	221	A
FGVRPQVPL	<u>293</u>	9	HIV	nef	84	A
FTVRPQVPL	<u>294</u>	9	HIV	nef	84	A
FSVRPQVPL	<u>295</u>	9	HIV	nef	84	A
YLKEPVHGV	<u>296</u>	9	HIV	pol	476	A
FLKEPVHGV	<u>297</u>	9	HIV	pol	476	
PVPLQLPPV	<u>298</u>	9	HIV	REV	74	A
LQLPPLERV	<u>299</u>	9	HIV	REV	77	A
LLLPLERLTL	<u>300</u>	11	HIV	REV	77	A

HLA-A2 SUPERTYPE

Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
LQLPPLERLTV	<u>301</u>	11	HIV	REV	77	A
ILWQVDRM	<u>302</u>	8	HIV	VIF	9	A
KLGSLLQYL	<u>303</u>	8	HIV	VIF	146	A
KVGSLLQYV	<u>304</u>	8	HIV	VIF	146	A
TLHDLQCQAV	<u>305</u>	9	HPV	E6	11	A
TLQDIVLHL	<u>306</u>	9	HPV	E7	7	
TLGPGPGHL	<u>307</u>	9	HPV	E7	7	A
TLQGPGPGL	<u>308</u>	9	HPV	E7	7	A
TLSFVCPWCV	<u>309</u>	10	HPV	E7	94	A
TLSFVCPWCA	<u>310</u>	10	HPV18	E7	93	
RTLHDLQCQA	<u>311</u>	9	HPV33	E6	10	
TLHDLQCQAL	<u>312</u>	9	HPV33	E6	11	
YLSGADLNL	<u>313</u>	9	Human	CEA	605	A
YLEPGPVTA	<u>314</u>	9	Human	gp100	280	
LLDGTATLRL	<u>315</u>	10	Human	gp100	457	
KVYGLSAFV	<u>316</u>	9	Human	Her2/neu	369	A
IISAVVAIL	<u>317</u>	9	Human	Her2/neu	654	A
ILSAVVGIL	<u>318</u>	9	Human	Her2/neu	654	A
IISAVVGFL	<u>319</u>	9	Human	Her2/neu	654	A
IISAVVGIV	<u>320</u>	9	Human	Her2/neu	654	A
KISAVVGIL	<u>321</u>	9	Human	Her2/neu	369	A
KIFAVVGIL	<u>322</u>	9	Human	Her2/neu	369	A
KIFASVAIL	<u>323</u>	9	Human	Her2/neu	369	A
ELVSEFSRV	<u>324</u>	9	Human	Her2/neu	971	A
VLVHPQWVV	<u>325</u>	9	Human	Kallikrein2	53	A
VLVHPQWVLTV	<u>326</u>	11	Human	Kallikrein2	53	A
DLMLRLSEP	<u>327</u>	11	Human	Kallikrein2	120	A
PLVCNGVLQGV	<u>328</u>	11	Human	Kallikrein2	216	A
VLVHPQWVLTV	<u>329</u>	11	Human	Kallikrein2	53	A
PLVCNGVLQGV	<u>330</u>	11	Human	Kallikrein2	216	A
QLGPGPGLMEV	<u>331</u>	11	Human	MAGE3	159	A
QLVGPGPGMEV	<u>332</u>	11	Human	MAGE3	159	A
QLVFGPGPGEV	<u>333</u>	11	Human	MAGE3	159	A
QLVFGPGPGV	<u>334</u>	11	Human	MAGE3	159	A
ALGIGILTV	<u>335</u>	9	Human	MART1	27	A
AMGIGILTV	<u>336</u>	9	Human	MART1	27	A
LLWQPIPV	<u>337</u>	8	Human	PAP	136	
LLGPGPGV	<u>338</u>	8	Human	PAP	136	A
VLAKELKFVTL	<u>339</u>	11	Human	PAP	30	
VLGPGPGFVTL	<u>340</u>	11	Human	PAP	30	A
VLGPGPGVTL	<u>341</u>	11	Human	PAP	30	A
VLAKGPGPGTL	<u>342</u>	11	Human	PAP	30	A
VLAKGPGPGTL	<u>343</u>	11	Human	PAP	30	A
TLMSAMTNV	<u>344</u>	9	Human	PAP	112	A
ILYSAHDTTV	<u>345</u>	10	Human	PAP	384	A
IVYSAHDTTV	<u>346</u>	10	Human	PAP	284	A
VTAKELKFV	<u>347</u>	9	Human	PAP	30	A
ITYSAHDTTV	<u>348</u>	10	Human	PAP	284	A
SLSLGFLV	<u>349</u>	9	Human	PAP		

HLA-A2 SUPERTYPE

Sequence	SEQ ID		AA	Organism	Protein	Position	Analog
	NO.						
SLSLGFLFLV	<u>350</u>		10	Human	PAP		
LLALFPPEGV	<u>351</u>		10	Human	PAP		
LVALFPPEGV	<u>352</u>		10	Human	PAP		
ALFPPEGVSV	<u>353</u>		10	Human	PAP		
GLHGQDLFGV	<u>354</u>		10	Human	PAP		
LLPPYASCHV	<u>355</u>		10	Human	PAP		
LLWQPIPVHV	<u>356</u>		10	Human	PAP		
MLLRLSEPV	<u>357</u>		9	Human	PSA	118	A
ALGTTCYV	<u>358</u>		8	Human	PSA	143	A
VLRLFVCFLI	<u>359</u>		10	Pf		2	
FLIFHFFLFL	<u>360</u>		10	Pf		9	
LIFHFFLFLL	<u>361</u>		10	Pf		10	
FLFLLYILFL	<u>362</u>		10	Pf		15	
RLPVICSFLV	<u>363</u>		10	Pf		32	
VICSFLVFLV	<u>364</u>		10	Pf		35	
FLVFLVFSNV	<u>365</u>		10	Pf		39	
MMIMIKFMGV	<u>366</u>		10	Pf		62	
FLLYILFLV	<u>367</u>		9	Pf		17	
VICSFLVFL	<u>368</u>		9	Pf		35	
ATYGIIIPV	<u>369</u>		9	Pf		159	
KIYKIIIWI	<u>370</u>		9	Pf		9	
YMIKKLLKI	<u>371</u>		9	Pf		23	
LMTLYQIQV	<u>372</u>		9	Pf		42	
FMGVIIYIMI	<u>373</u>		9	Pf		68	
FMNRFYITT	<u>374</u>		9	Pf		312	
YQDPQNYEL	<u>375</u>		9	Pf		22	
KTWKPTIFL	<u>376</u>		9	Pf		134	
LLNESNIFL	<u>377</u>		9	Pf		142	
FIHFFTWTGT	<u>378</u>		9	Pf		220	
VLFLQMMNV	<u>379</u>		9	Pf		180	
NQMIFVSSI	<u>380</u>		9	Pf		251	
MIFVSSIFI	<u>381</u>		9	Pf		253	
SIFISFYLI	<u>382</u>		9	Pf		258	
RLFEESLGI	<u>383</u>		9	Pf		293	
ALWGFFPVL	<u>384</u>		9	Unknown	A2 alloepitope TRP2		A
SVYDFFVWL	<u>385</u>		9			180	
FAPGFFPYL	<u>386</u>		9				
QLFEDKYAL	<u>387</u>		9				
MLLSVPLLL	<u>388</u>		9				

TABLE 14

HLA-A2 SUPERTYPE						
Sequence	SEQ ID NO.	A*0201	A*0202	A*0203	A*0206	A*6802
FPFKYAAAV	<u>206</u>					92
AMAKAAAAV	<u>207</u>	181	196	6.7	1485	177
AMAKAAAAL	<u>208</u>	413	123	3.7	18500	320
AMAKAAAAT	<u>209</u>	15143	12413	84	37000	>26666.67
AXAKAAAAL	<u>210</u>	>50000	469	3300	37000	>11428.57
FVYGGSKTSL	<u>211</u>	296				
ILGPGPGL	<u>212</u>	672	45	530	1262	56099
GILGFVFTL	<u>213</u>	1.0	10	236	2.1	1395
GLIYNRMGAV	<u>214</u>	317				
VLMEWLKTRPI	<u>215</u>	464				
FLPSDYFPSV	<u>216</u>	8.5	3.3	3.2	2.2	276
FLGPGPGPSV	<u>217</u>	17	0.80	2.5	55	286
FLPGPGPGSV	<u>218</u>	98	18	4.0	665	332
FLPSGPGPGV	<u>219</u>	21	1.2	3.4	64	40
WLGPGPGFV	<u>220</u>	171	4.1	2.2	530	293
WLSGPGPGV	<u>221</u>	220	2.5	12	885	24
GVLGWSPQV	<u>222</u>	22	157	389	28	9428
PVLPIFFCV	<u>223</u>	8.7	3136	14286	22	1814
VVQAGFFLV	<u>224</u>	440	79	2503	81	617
FLLAQFTSAI	<u>225</u>	65	1.9	4.8	148	533
YLLTLWKAGI	<u>226</u>	20	19	20	40	1388
YLGPGPGAGI	<u>227</u>	161	1.0	4.2	548	315
YLLGPGPGGI	<u>228</u>	180	12	3.3	89	2064
YLLTGPGPGI	<u>229</u>	42	15	59	60	5678
HVYSHPIIV	<u>230</u>	150	1923	14	1199	123
FVLSLGIHV	<u>231</u>	45	399	2817	131	112
YVDDVVLGV	<u>232</u>	18	14	70	16	354
IVRGTSFVYV	<u>233</u>	50000	5301	69	5398	1217
SLGPGPGIAV	<u>234</u>	1131	5.3	11	917	281
SLLGPGPGAV	<u>235</u>	95	17	2.6	642	795
SLLNGPGPGV	<u>236</u>	65	3.8	14	63	45
KITPLCVTL	<u>237</u>	461	36	528	59	883
KLTPLCVTM	<u>238</u>	340	3.6	143	197	6288
KLTPLCVPL	<u>239</u>	15	0.25	297	135	67
KLTPLCVSL	<u>240</u>	67	2.4	240	16	5947
KLTPLCITL	<u>241</u>	1.7	0.27	23	1.7	9155
QLTPLCVTL	<u>242</u>	64	1.5	57	368	933
KLTPRCVTL	<u>243</u>	597	150	20	1554	>63492.06
ELTPLCVTL	<u>244</u>	7190	38	231	1919	32
QMTFLCVQM	<u>245</u>	3153	40	1127	232	1297
KMTFLCVQM	<u>246</u>	1793	22	525	100	8744
KLTPLCVAL	<u>247</u>	209	2.3	54	11	13009
KLTPFCVTL	<u>248</u>	87	0.37	28	78	11814
SLYNTVATL	<u>249</u>	290	6573	68	37000	20000
VLAEAMSQT	<u>250</u>	290	2.2	0.65	236	447

HLA-A2 SUPERTYPE						
Sequence	SEQ ID NO.	A*0201	A*0202	A*0203	A*0206	A*6802
VLAEAMSQA	<u>251</u>	24	1.1	0.30	9.6	271
VLAEAMSQI	<u>252</u>	71	0.15	0.87	70	207
ILAEAMSQV	<u>253</u>	38	1.1	1.1	101	34
VLAEAMSKV	<u>254</u>	230	1.8	1.4	93	329
VLAEAMSHA	<u>255</u>	149	1.7	1.2	121	431
ILAEAMSQA	<u>256</u>	29	1.0	1.1	8.6	253
VLAEAMSRA	<u>257</u>	127	0.88	1.0	20	229
VLAEAMATA	<u>258</u>	6.7	1.4	0.73	8.6	33
ILAEAMASA	<u>259</u>	22	0.72	0.82	6.8	343
MTHNPPIPV	<u>260</u>	167	119	1.4	158	1.4
MTNPPVPV	<u>261</u>	86	18	0.42	287	309
MTSNPPIPV	<u>262</u>	53	16	0.39	250	3.8
MTSNPPVPV	<u>263</u>	22	29	0.80	81	1.1
MTSDPPIPV	<u>264</u>	107	13	0.45	587	2.5
MTGNPPIPV	<u>265</u>	125	11	0.74	79	7.8
MTGNPPVPV	<u>266</u>	2021	158	23	35	0.84
MTGNPAIPV	<u>267</u>	1200	24	10	213	0.48
MTGNPSIPV	<u>268</u>	16	1.1	0.43	257	0.57
MTANPPVPV	<u>269</u>	20	5.0	0.62	134	4.0
SLYNTVATL	<u>270</u>	367	79	19	15072	247113
QAHCNISRA	<u>271</u>	338				
FLKEKGGV	<u>272</u>	13327	653	267	>14341.09	>19464.72
GLGAVSRDL	<u>273</u>	18679	436	1733	>10393.26	>16666.67
GLITSSNTA	<u>274</u>	5800	102	64	7865	>14311.27
ALEEEVGFPV	<u>275</u>	2420	487	15744	2988	>13793.1
FLKEKGGLGV	<u>276</u>	322	3.5	6.8	739	1252
FLKEKGGLDGV	<u>277</u>	332	3.7	11	3207	3807
GLIYSKKRQEV	<u>278</u>	8971	57	152	>8564.81	>14260.25
LLYSKKRQEI	<u>279</u>	80687	382	152	>9438.78	>15686.27
LLYSKKRQEIL	<u>280</u>	>38167.9	282	1569	>8564.81	>14260.25
RLDILDLWV	<u>281</u>	43	615	1639	2635	>17777.78
EILDLWVYHV	<u>282</u>	496	569	1865	2229	163
ILDLWVYHV	<u>283</u>	17	30	156	145	7414
ILDLWVYNV	<u>284</u>	40	30	201	135	5814
WLNYTPGPGT	<u>285</u>	547	124	231	>31623.93	11808
WQNYTPGPGV	<u>286</u>	1175	114	230	223	11993
WLNYTPGPGI	<u>287</u>	135	4.6	46	>31623.93	1196
YLPGPGRYPV	<u>288</u>	1026	20	1583	3497	782
YTPGPGRYPV	<u>289</u>	7764	1985	11126	1112	9.2
LLFGWCFKL	<u>290</u>	18	4.1	198	340	1084
LTFGWCFKV	<u>291</u>	15	33	1168	187	9.7
LLFGWCFKLV	<u>292</u>	658	84	114	1669	3276
FGVRPQVPL	<u>293</u>					321
FTVRPQVPL	<u>294</u>					13
FSVRPQVPL	<u>295</u>					52
YLKEPVHGV	<u>296</u>	54	0.65	1.9	212	63
FLKEPVHGV	<u>297</u>	44	0.28	1.9	140	135

HLA-A2 SUPERTYPE						
Sequence	SEQ ID NO.	A*0201	A*0202	A*0203	A*0206	A*6802
PVPLQLPPV	<u>298</u>	10047	>7337.88	12595	81	>15625
LQLPPLERV	<u>299</u>	7951	7705	13517	203	1786
LLLPPLERLTL	<u>300</u>	34	2607	9010	45	>12779.55
LQLPPLERLTV	<u>301</u>	159	4545	6270	52	>61068.7
ILWQVDRM	<u>302</u>	1745	67	2998	11332	>19464.72
KLGSLQYL	<u>303</u>	1862	14	298	9010	>19464.72
KVGSLQYV	<u>304</u>	1650	441	703	1904	17480
TLHDLCQAV	<u>305</u>	331	17	15	10585	2809
TLQDIVLHL	<u>306</u>	22	4.4	46	781	5088
TLGPGPGHL	<u>307</u>	14974	35	66	12144	27910
TLQGPGL	<u>308</u>	6248	62	951	9121	3809
TLSFVCPWCV	<u>309</u>	786	123	370	4357	388
TLSFVCPWCA	<u>310</u>	1611	221	521	27321	13228
RTLHDLCQA	<u>311</u>	8121	34	678	96	61604
TLHDLCQAL	<u>312</u>	1404	2.7	40	2182	70390
YLSGADLNL	<u>313</u>	36	4.9	9.2	1605	51227
YLEPGPVTA	<u>314</u>	466	10	27	20720	>470588.2 4
LLDGTATLRL	<u>315</u>	180	1.9	201	841	>421052.6 3
KVYGLSAFV	<u>316</u>	33	1.8	11	69	110
IISAVVAIL	<u>317</u>	1127	8.0	45	1440	148
ILSAVVGIL	<u>318</u>	1464	1.9	21	2539	11854
IISAVVGFL	<u>319</u>	747	1.0	4.8	234	77
IISAVVGIV	<u>320</u>	712	15	20	958	390
KISAVVGIL	<u>321</u>	6238	42	60	1752	4952
KIFAVVGIL	<u>322</u>	3957	38	34	1539	6659
KIFASVAIL	<u>323</u>	1062	16	21	1068	363
ELVSEFSRV	<u>324</u>	8178	969	53	197	23
VLVHPQWVV	<u>325</u>	464	65	1988	3224	14606
VLVHPQWVLT V	<u>326</u>	11	1.7	3.0	13	3288
DLMLLRLSEPV	<u>327</u>	69	66	32	118	2078
PLVCNGVLQGV	<u>328</u>	91	424	36	212	3532
VLVHPQWVLT V	<u>329</u>	11	1.5	16	31	8889
PLVCNGVLQGV	<u>330</u>	26	126	19	264	4211
QLGPGPGLMEV	<u>331</u>	194	9.4	29	481	648
QLVGPGPGMEV	<u>332</u>	865	17	19	919	223
QLVFGPGPGEV	<u>333</u>	2944	106	50	4067	447
QLVFGGPGPGV	<u>334</u>	2153	96	242	3207	1318
ALGIGILTV	<u>335</u>	11				
AMGIGILTV	<u>336</u>	15				
LLWQPIPV	<u>337</u>	137	2445	9.9	4251	32939
LLGPGPGV	<u>338</u>	25	49	123	93	5620
VLAKELKFVTL	<u>339</u>	1298	23	194	5170	15664
VLGPGPGFVTL	<u>340</u>	1528	13	63	4766	42136
VLAGPGPGVTL	<u>341</u>	1118	2.4	94	7200	2645
VLAKGPGPGTL	<u>342</u>	11256	26	344	11450	>170212.7

HLA-A2 SUPERTYPE						
Sequence	SEQ ID NO.	A*0201	A*0202	A*0203	A*0206	A*6802
						7
VLAKEGPGPGL	<u>343</u>	1890	6.9	37	59024	50993
TLMSAMTNV	<u>344</u>	636	14	35	2188	484
ILYSAHDTTV	<u>345</u>	397	1.1	13	1480	6285
IVYSAHDTTV	<u>346</u>	7643	91	627	356	737
VTAKELKFV	<u>347</u>	7143	2688	40	137	26667
ITYSAHDTTV	<u>348</u>	4167	115	238	154	82
SLSLGFLFV	<u>349</u>	77	25	21	93	26667
SLSLGFLFLV	<u>350</u>	1.9	3.9	17	42	348
LLALFPPEGV	<u>351</u>	5.0	0.73	1.6	148	163
LVALFPPEGV	<u>352</u>	156	17	4.8	463	28
ALFPPEGVSV	<u>353</u>	15	1.1	18	119	4444
GLHGQDLFGV	<u>354</u>	12	2.3	3.1	18	>80000
LLPPYASCHV	<u>355</u>	88	15	16	97	5333
LLWQIPVHV	<u>356</u>	25	1.8	18	285	62
MLLRLSEPV	<u>357</u>	47	29	48	689	433
ALGTTCYV	<u>358</u>	93	6.7	12	292	28284
VLRLFVCFLI	<u>359</u>	2744	2112	299	68226	45639
FLIFHFFLFL	<u>360</u>	161	174	2087	288	475
LIFHFFLFL	<u>361</u>	200	1468	3167	1562	460
FLFLLYILFL	<u>362</u>	2834	172	2012	2113	8248
RLPVICSFLV	<u>363</u>	12	2.5	33	19	9176
VICSFLVFLV	<u>364</u>	167	415	2916	197	1949
FLVFLVFSNV	<u>365</u>	269	212	35	232	5393
MMIMIKFMGV	<u>366</u>	123	19	25	109	39
FLLYILFLV	<u>367</u>	346	279	3091	1801	6981
VICSFLVFL	<u>368</u>	184	19	2331	236	4800
ATYGIIVPV	<u>369</u>	3.2	2.0	2.8	5.0	21
KIYKHIWI	<u>370</u>	157	1179	638	101	2198
YMIKKLLKI	<u>371</u>	105	4.6	4.7	93	63127
LMTLYQIQV	<u>372</u>	14	1.6	20	615	1276
FMGVIIYIMI	<u>373</u>	13	2.1	26	98	14501
FMNRFYITT	<u>374</u>	101	18	13	996	6543
YQDPQNYEL	<u>375</u>	79	18	441	52	166775
KTWKPTIFL	<u>376</u>	135	1242	7487	76	3617
LLNESNIFL	<u>377</u>	43	2.5	24	143	4484
FIHFFTWT	<u>378</u>	80	4.7	64	60	383
VLFLQMMNV	<u>379</u>	31	1.8	2.7	9.5	323
NQMIFVSSI	<u>380</u>	250	21	3.6	14	198
MIFVSSIFI	<u>381</u>	85	18	83	114	5.2
SIFISFYLI	<u>382</u>	289	35	1416	43	18
RLFEESLGI	<u>383</u>	26	1.9	5.5	68	418
ALWGFFPVL	<u>384</u>	3.6	0.74	3.7	15	1503
SVYDFFVWL	<u>385</u>	36	169	226	10	0.86
FAPGFFPYL	<u>386</u>	48	0.85	44	2.3	7.6
QLFEDKYAL	<u>387</u>	646	1.8	380	2009	2982
MLLSVPLLL	<u>388</u>	9.0	79	41	8.4	24607

TABLE 15

HLA-A3 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
ALNAAAAAK	<u>389</u>	9	Artificial sequence			Poly
ALAAGAAAK	<u>390</u>	9	Artificial sequence			Poly
ALQAAAAAK	<u>391</u>	9	Artificial sequence			Poly
STGPGPGVRR	<u>392</u>	11	HBV	core	141	A
STLPGPGVRR	<u>393</u>	11	HBV	core	141	A
STLPGPGGR	<u>394</u>	11	HBV	core	141	A
STLPGPGPR	<u>395</u>	11	HBV	core	141	A
QAGFFLLTR	<u>396</u>	9	HBV	ENV	179	
RVHFASPLH	<u>397</u>	9	HBV	POL	818	
AAAYAAQGYK	<u>398</u>	9	HCV	II	1247	
KSKFGYGAK	<u>399</u>	9	HCV	II	2551	
PAAYAAQGYK	<u>400</u>	10	HCV	II	1246	
RMVVGVEH	<u>401</u>	9	HCV	IV	635	
SQLSAPSLK	<u>402</u>	9	HCV	IV	2209	
TSCGNTLTCTY	<u>403</u>	10	HCV	NS5	2740	
VTGPGPGPVWK	<u>404</u>	11	HIV	env	48	A
VTGPGPGVWK	<u>405</u>	11	HIV	env	48	A
VTVYGPVGWK	<u>406</u>	11	HIV	env	48	A
VTVYGPVGPK	<u>407</u>	11	HIV	env	48	A
PVRPQVPLR	<u>408</u>	9	HIV	NEF	95	
HGAITSSNTK	<u>409</u>	10	HIV	NEF	61	A
AVDLSFFLK	<u>410</u>	9	HIV	NEF	111	A
DVSHFLKEK	<u>411</u>	9	HIV	NEF	113	A
GVL DGLIYSK	<u>412</u>	10	HIV	NEF	124	A
GVDGLIYSK	<u>413</u>	9	HIV	NEF	125	A
EILDWVYK	<u>414</u>	9	HIV	NEF	185	A
ILDWVYK	<u>415</u>	8	HIV	NEF	186	A
RVPLTFGWCFK	<u>416</u>	11	HIV	NEF	216	A
QVYTPGPGTR	<u>417</u>	10	HIV	NEF	205	A
AVGPGPGLK	<u>418</u>	9	HIV	nef	84	A
AVDGP GPK	<u>419</u>	9	HIV	nef	84	A
QMGP GPNFK	<u>420</u>	10	HIV	pol	1432	A
QMAGPGPGFK	<u>421</u>	10	HIV	pol	1432	A
QMAVGPGPGK	<u>422</u>	10	HIV	pol	1432	A
TVGPGPGPEK	<u>423</u>	10	HIV	pol	935	A
TVQGP GGEK	<u>424</u>	10	HIV	pol	935	A
TVQGP GPGK	<u>425</u>	10	HIV	pol	935	A
VAIKIGGQLK	<u>426</u>	10	HIV	Pol	98	A
VTVKIGGQLK	<u>427</u>	10	HIV	Pol	98	A
VTIKVGGQLK	<u>428</u>	10	HIV	Pol	98	A
VTIRIGGQLK	<u>429</u>	10	HIV	Pol	98	A
VTVRIGGQLK	<u>430</u>	10	HIV	Pol	98	A
VTVKVGGQLK	<u>431</u>	10	HIV	Pol	98	A
VTIRVGGQLK	<u>432</u>	10	HIV	Pol	98	A

HLA-A3 SUPERTYPE						
Sequence	SEQ ID		Organism	Protein	Position	Analog
	NO.	AA				
VTVRVGGQLK	<u>433</u>	10	HIV	Pol	98	A
VTVKIGGQLR	<u>434</u>	10	HIV	Pol	98	A
VTIRIGGQLR	<u>435</u>	10	HIV	Pol	98	A
VTIKLGGQIR	<u>436</u>	10	HIV	Pol	98	A
VSIKVGGQIK	<u>437</u>	10	HIV	Pol	98	A
VSIRVGGQIK	<u>438</u>	10	HIV	Pol	98	A
VTVKIEGQLK	<u>439</u>	10	HIV	Pol	98	A
VTIKIEGQLK	<u>440</u>	10	HIV	Pol	98	A
VTVKIEGQLR	<u>441</u>	10	HIV	Pol	98	A
VSIRVGGQTK	<u>442</u>	10	HIV	Pol	98	A
VSIRVGGQTR	<u>443</u>	10	HIV	Pol	98	A
VTVRIGGMQK	<u>444</u>	10	HIV	Pol	98	A
ITVKIGKEVR	<u>445</u>	10	HIV	Pol	98	A
GTRQARRNK	<u>446</u>	9	HIV	REV	36	A
GTRQARRNRK	<u>447</u>	10	HIV	REV	36	A
GTRQARRNRRK	<u>448</u>	11	HIV	REV	36	A
GTRQTRKNK	<u>449</u>	9	HIV	REV	37	A
GTRQTRKNRK	<u>450</u>	10	HIV	REV	37	A
GTRQTRKNRRK	<u>451</u>	11	HIV	REV	37	A
RVRRRRWRAR	<u>452</u>	10	HIV	REV	43	A
KVRRRRWRAR	<u>453</u>	10	HIV	REV	43	A
LTISYGRK	<u>454</u>	8	HIV	TAT	46	A
KTLGISYGR	<u>455</u>	9	HIV	TAT	44	A
LTISYGRKK	<u>456</u>	9	HIV	TAT	46	A
GTSYGRKKR	<u>457</u>	9	HIV	TAT	47	A
GTGISYGRK	<u>458</u>	9	HIV	TAT	45	A
KTLGISYGRK	<u>459</u>	10	HIV	TAT	44	A
LTISYGRKKR	<u>460</u>	10	HIV	TAT	46	A
KTLGISYGRKK	<u>461</u>	11	HIV	TAT	44	A
TVCNNCYCK	<u>462</u>	9	HIV	TAT	23	A
LVISYGRKKRR	<u>463</u>	11	HIV	TAT	46	A
ISYGRKKRRQK	<u>464</u>	11	HIV	TAT	48	A
ETGPGSQPCK	<u>465</u>	10	HIV	TAT	101	A
KVGPGGYPRR	<u>466</u>	10	HIV	TAT	101	A
KAGPGGYPRK	<u>467</u>	10	HIV	TAT	101	A
KVGPGGYPRRK	<u>468</u>	11	HIV	TAT	101	A
AVPGGYPRR	<u>469</u>	9	HIV	TAT	102	A
AVPGGYPRRK	<u>470</u>	10	HIV	TAT	102	A
KVGSLQYLK	<u>471</u>	9	HIV	VIF	146	A
ETVRHFPR	<u>472</u>	8	HIV	VPR	29	A
AACHKCIDFY	<u>473</u>	10	HPV	E6	63	
LLIRCLRCQK	<u>474</u>	10	HPV	E6	101	
KISEYRHYN	<u>475</u>	10	HPV	E6	72	
AVCRVCLLFY	<u>476</u>	10	HPV	E6	64	
FAFTDLTIVY	<u>477</u>	10	HPV	E6	45	
FAFADLTVVY	<u>478</u>	10	HPV	E6	45	
RFLSKISEYR	<u>479</u>	10	HPV	E6	68	
ILIRCIICQR	<u>480</u>	10	HPV	E6	99	
RTAMFQDPQER	<u>481</u>	11	HPV	E6	5	

HLA-A3 SUPERTYPE						
Sequence	SEQ ID		Organism	Protein	Position	Analog
	NO.	AA				
AMFQDPQERPR	<u>482</u>	11	HPV	E6	7	
MFQDPQERPRK	<u>483</u>	11	HPV	E6	8	
DLLIRCINCQK	<u>484</u>	11	HPV	E6	105	
RFEDPTRRPYK	<u>485</u>	11	HPV	E6	3	
ELTEVFFAFK	<u>486</u>	11	HPV	E6	40	
GLYNLLIRCLR	<u>487</u>	11	HPV	E6	97	
NLLIRCLRCQK	<u>488</u>	11	HPV	E6	100	
EVLEESVHEIR	<u>489</u>	11	HPV	E6	17	
EVYKFLFTDLR	<u>490</u>	11	HPV	E6	41	
FLFTDLRIVYR	<u>491</u>	11	HPV	E6	45	
EVLEIPLIDLR	<u>492</u>	11	HPV	E6	20	
DLRLSCVYCKK	<u>493</u>	11	HPV	E6	28	
EVYNFACTELK	<u>494</u>	11	HPV	E6	44	
RVCLLFYSKVR	<u>495</u>	11	HPV	E6	67	
LLFYSKVRKYR	<u>496</u>	11	HPV	E6	70	
QLCDLLIRCYR	<u>497</u>	11	HPV	E6	98	
TLEQTVKK	<u>498</u>	8	HPV	E6	87	
ATRDLCIVYR	<u>499</u>	10	HPV	E6	53	A
AFRDL CIVYK	<u>500</u>	10	HPV	E6	53	A
ATCDKCLKFY	<u>501</u>	10	HPV	E6	68	A
AVCDKCLKFR	<u>502</u>	10	HPV	E6	68	A
KLYSKISEYR	<u>503</u>	10	HPV	E6	75	A
KFYSKISEYK	<u>504</u>	10	HPV	E6	75	A
KFSEYRHICY	<u>505</u>	10	HPV	E6	79	A
KISEYRHYCR	<u>506</u>	10	HPV	E6	79	A
LFIRCINCQK	<u>507</u>	10	HPV	E6	106	A
LLIRCINCQR	<u>508</u>	10	HPV	E6	106	A
KVRFHNIRGR	<u>509</u>	10	HPV	E6	129	A
KQRFHNIRGK	<u>510</u>	10	HPV	E6	129	A
WFGRCMSSCR	<u>511</u>	10	HPV	E6	139	A
WTGRCMSCKK	<u>512</u>	10	HPV	E6	139	A
MTCCRSSRTR	<u>513</u>	10	HPV	E6	144	A
MSCCRSSRTK	<u>514</u>	10	HPV	E6	144	A
STCRSSRTRR	<u>515</u>	10	HPV	E6	145	A
SCCRSSRTRK	<u>516</u>	10	HPV	E6	145	A
DIEITCVYCR	<u>517</u>	10	HPV	E6	27	A
FTFKDLFVVY	<u>518</u>	10	HPV	E6	47	A
FAFKDLFVVK	<u>519</u>	10	HPV	E6	47	A
AVKDLFVVYR	<u>520</u>	10	HPV	E6	48	A
AFKDLFVVYK	<u>521</u>	10	HPV	E6	48	A
FVVYRDSIPK	<u>522</u>	10	HPV	E6	53	A
DTIPHAACHK	<u>523</u>	10	HPV	E6	58	A
DSIPHAACHR	<u>524</u>	10	HPV	E6	58	A
KFIDFYSRIR	<u>525</u>	10	HPV	E6	67	A
DTVYGDITLEK	<u>526</u>	10	HPV	E6	83	A
DSVYGDTLER	<u>527</u>	10	HPV	E6	83	A
LFIRCLRCQK	<u>528</u>	10	HPV	E6	101	A
LLIRCLRCQR	<u>529</u>	10	HPV	E6	101	A
RVHNIAGHYR	<u>530</u>	10	HPV	E6	126	A

HLA-A3 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
RFHNIAGHYK	<u>531</u>	10	HPV	E6	126	A
RTQCHSCCNR	<u>532</u>	10	HPV	E6	135	A
RGQCHSCCNK	<u>533</u>	10	HPV	E6	135	A
ATDILTIVYR	<u>534</u>	10	HPV	E6	46	A
AFTDILTIVYK	<u>535</u>	10	HPV	E6	46	A
RLYSKVSEFR	<u>536</u>	10	HPV	E6	68	A
RFYSKVSEFK	<u>537</u>	10	HPV	E6	68	A
KFSEFRWYRY	<u>538</u>	10	HPV	E6	72	A
KVSEFRWYRR	<u>539</u>	10	HPV	E6	72	A
YFVYGTITLEK	<u>540</u>	10	HPV	E6	81	A
YSVYGTTLER	<u>541</u>	10	HPV	E6	81	A
GTTLEKLTNR	<u>542</u>	10	HPV	E6	85	A
LVIRCITCQR	<u>543</u>	10	HPV	E6	99	A
LLIRCITCQK	<u>544</u>	10	HPV	E6	99	A
WVGRCIACWR	<u>545</u>	10	HPV	E6	132	A
WTGRCIACWK	<u>546</u>	10	HPV	E6	132	A
RTIACWRRPR	<u>547</u>	10	HPV	E6	135	A
RCIACWRRPK	<u>548</u>	10	HPV	E6	135	A
AVADLTVVYR	<u>549</u>	10	HPV	E6	46	A
AFADLTVVYK	<u>550</u>	10	HPV	E6	46	A
RVLSKISEYR	<u>551</u>	10	HPV	E6	68	A
RFLSKISEYK	<u>552</u>	10	HPV	E6	68	A
KFSEYRHYN	<u>553</u>	10	HPV	E6	72	A
KISEYRHYNR	<u>554</u>	10	HPV	E6	72	A
ITIRCIICQR	<u>555</u>	10	HPV	E6	99	A
ILIRCIICQK	<u>556</u>	10	HPV	E6	99	A
WVGRCIACWR	<u>557</u>	10	HPV	E6	132	A
WAGRCIACWK	<u>558</u>	10	HPV	E6	132	A
CFACWRSRRR	<u>559</u>	10	HPV	E6	136	A
DTSIACVYCK	<u>560</u>	10	HPV	E6	27	A
DVSIACVYCR	<u>561</u>	10	HPV	E6	27	A
CVYCKATLEK	<u>562</u>	10	HPV	E6	32	A
RFEVYQFAFK	<u>563</u>	10	HPV	E6	41	A
RTEVYQFAFR	<u>564</u>	10	HPV	E6	41	A
AVKDLICIVYR	<u>565</u>	10	HPV	E6	48	A
AFKDLICIVYK	<u>566</u>	10	HPV	E6	48	A
ATCHKCIDFY	<u>567</u>	10	HPV	E6	63	A
AACHKCIDFK	<u>568</u>	10	HPV	E6	63	A
NLVYGETLEK	<u>569</u>	10	HPV	E6	83	A
NSVYGETLER	<u>570</u>	10	HPV	E6	83	A
LSIRCLRCQK	<u>571</u>	10	HPV	E6	101	A
LLIRCLRCQY	<u>572</u>	10	HPV	E6	101	A
RVHSIAGQYR	<u>573</u>	10	HPV	E6	126	A
RFHSIAGQYK	<u>574</u>	10	HPV	E6	126	A
LVTDLRIVYR	<u>575</u>	10	HPV	E6	46	A
LFTDLRIVYK	<u>576</u>	10	HPV	E6	46	A
CTMCLRFLSK	<u>577</u>	10	HPV	E6	63	A
CIMCLRFLSR	<u>578</u>	10	HPV	E6	63	A
RLLSKISEYR	<u>579</u>	10	HPV	E6	68	A

HLA-A3 SUPERTYPE						
Sequence	SEQ ID		Organism	Protein	Position	Analog
	NO.	AA				
RFLSKISEYY	<u>580</u>	10	HPV	E6	68	A
SFYGKTLEER	<u>581</u>	10	HPV	E6	82	A
SLYGKTLEEK	<u>582</u>	10	HPV	E6	82	A
WFGRCSECWR	<u>583</u>	10	HPV	E6	132	A
WTGRCSECWK	<u>584</u>	10	HPV	E6	132	A
AFCRVCLLFY	<u>585</u>	10	HPV	E6	64	A
AVCRVCLLFR	<u>586</u>	10	HPV	E6	64	A
CFLFYSKVRK	<u>587</u>	10	HPV	E6	69	A
CLLFYSKVRR	<u>588</u>	10	HPV	E6	69	A
LVYSKVRKYR	<u>589</u>	10	HPV	E6	71	A
LFYSKVRKYK	<u>590</u>	10	HPV	E6	71	A
GTTLESITKK	<u>591</u>	10	HPV	E6	88	A
WVGSCLCGWR	<u>592</u>	10	HPV	E6	135	A
WTGSCLCGWK	<u>593</u>	10	HPV	E6	135	A
VVADLRIVYR	<u>594</u>	10	HPV	E6	46	A
VFADLRIVYK	<u>595</u>	10	HPV	E6	46	A
RTLSKISEYR	<u>596</u>	10	HPV	E6	68	A
RLLSKISEYK	<u>597</u>	10	HPV	E6	68	A
KVSEYRHYNY	<u>598</u>	10	HPV	E6	72	A
KISEYRHYNK	<u>599</u>	10	HPV	E6	72	A
IVIRCHICQR	<u>600</u>	10	HPV	E6	99	A
WLGRCAVCWR	<u>601</u>	10	HPV	E6	132	A
WTGRCAVCWK	<u>602</u>	10	HPV	E6	132	A
YVVCCKCLK	<u>603</u>	9	HPV	E6	67	A
YAVCDKCLR	<u>604</u>	9	HPV	E6	67	A
SVCRSSRTR	<u>605</u>	9	HPV	E6	145	A
SCCRSSRTK	<u>606</u>	9	HPV	E6	145	A
SLPHAACHK	<u>607</u>	9	HPV	E6	59	A
SIPHAACHR	<u>608</u>	9	HPV	E6	59	A
FVDLTIVYR	<u>609</u>	9	HPV	E6	47	A
FTDLTIVYK	<u>610</u>	9	HPV	E6	47	A
SFYGTTLEK	<u>611</u>	9	HPV	E6	82	A
SVYGTTLER	<u>612</u>	9	HPV	E6	82	A
TFLEKLTNK	<u>613</u>	9	HPV	E6	86	A
TTLEKLTNR	<u>614</u>	9	HPV	E6	86	A
ETNPFGICK	<u>615</u>	9	HPV	E6	56	A
EGNPFGICR	<u>616</u>	9	HPV	E6	56	A
NTLEQTVKR	<u>617</u>	9	HPV	E6	86	A
ALCWRSRRR	<u>618</u>	9	HPV	E6	137	A
AACWRSRRK	<u>619</u>	9	HPV	E6	137	A
VSIACVYCR	<u>620</u>	9	HPV	E6	28	A
SIACVYCKK	<u>621</u>	9	HPV	E6	29	A
ILYRDCIAY	<u>622</u>	9	HPV	E6	54	A
IVYRDCIAR	<u>623</u>	9	HPV	E6	54	A
CTAYAACHK	<u>624</u>	9	HPV	E6	59	A
CIAYAACHR	<u>625</u>	9	HPV	E6	59	A
SFYGETLEK	<u>626</u>	9	HPV	E6	84	A
SVYGETLER	<u>627</u>	9	HPV	E6	84	A
LIRCLRCQR	<u>628</u>	9	HPV	E6	102	A

HLA-A3 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
RTQCVQCKK	<u>629</u>	9	HPV	E6	27	A
RLQCVQCKR	<u>630</u>	9	HPV	E6	27	A
KFLEERVKK	<u>631</u>	9	HPV	E6	86	A
KTLEERVKR	<u>632</u>	9	HPV	E6	86	A
NVMGRWTGR	<u>633</u>	9	HPV	E6	127	A
NIMGRWTGK	<u>634</u>	9	HPV	E6	127	A
LTYRDDFPY	<u>635</u>	9	HPV	E6	55	A
LVYRDDFPK	<u>636</u>	9	HPV	E6	55	A
RFCLLFYSK	<u>637</u>	9	HPV	E6	67	A
RVCLLFYSR	<u>638</u>	9	HPV	E6	67	A
LTFYSKVRK	<u>639</u>	9	HPV	E6	70	A
LLFYSKVRR	<u>640</u>	9	HPV	E6	70	A
ATLESITKR	<u>641</u>	9	HPV	E6	89	A
KVLCDLLIR	<u>642</u>	9	HPV	E6	97	A
KQLCDLLIK	<u>643</u>	9	HPV	E6	97	A
TFVHEIELK	<u>644</u>	9	HPV	E6	21	A
TSVHEIELR	<u>645</u>	9	HPV	E6	21	A
YTFVFADLR	<u>646</u>	9	HPV	E6	43	A
DFLEQTLKK	<u>647</u>	9	HPV	E6	86	A
DTLEQTLKR	<u>648</u>	9	HPV	E6	86	A
LVRCHCQR	<u>649</u>	9	HPV	E6	100	A
LIRCHCQK	<u>650</u>	9	HPV	E6	100	A
RVAVCWRPR	<u>651</u>	9	HPV	E6	135	A
RCAVCWRPK	<u>652</u>	9	HPV	E6	135	A
AFCWRPRRR	<u>653</u>	9	HPV	E6	137	A
AVCWRPRRK	<u>654</u>	9	HPV	E6	137	A
LSFVCPWCA	<u>655</u>	9	HPV	E7	94	
TFCKCDSTLR	<u>656</u>	11	HPV	E7	56	
LVVSSADDLR	<u>657</u>	11	HPV	E7	74	
TLQVVCPCAR	<u>658</u>	11	HPV	E7	88	
YLIHVPCCECK	<u>659</u>	11	HPV	E7	59	
FVVQLDIQSTK	<u>660</u>	11	HPV	E7	70	
HTCNTTVR	<u>661</u>	8	HPV	E7	59	
GLVCPICSQK	<u>662</u>	10	HPV	E7	88	A
GFNHQHLPAR	<u>663</u>	10	HPV	E7	43	A
GVNHQHLPAR	<u>664</u>	10	HPV	E7	43	A
NVVTFCQCK	<u>665</u>	10	HPV	E7	53	A
NIVTFCCQCR	<u>666</u>	10	HPV	E7	53	A
GVSHAQLPAK	<u>667</u>	10	HPV	E7	44	A
LIHVPCCECR	<u>668</u>	10	HPV	E7	60	A
AVLQDIVLH	<u>669</u>	9	HPV	E7	6	A
ATLQDIVLK	<u>670</u>	9	HPV	E7	6	A
GVNHQHLPK	<u>671</u>	9	HPV	E7	43	A
HVMLCMCKK	<u>672</u>	9	HPV	E7	59	A
HTMLCMCCR	<u>673</u>	9	HPV	E7	59	A
LSFVCPWCR	<u>674</u>	9	HPV	E7	94	A
AQPATADYK	<u>675</u>	9	HPV	E7	45	A
VVHAQLPAR	<u>676</u>	9	HPV	E7	45	A
VSHAQLPAK	<u>677</u>	9	HPV	E7	45	A

HLA-A3 SUPERTYPE						
Sequence	SEQ ID		Organism	Protein	Position	Analog
	NO.	AA				
QLARQAKQH	<u>678</u>	9	HPV	E7	48	A
KQHTCYLIR	<u>679</u>	9	HPV	E7	54	A
VTLDIQSTK	<u>680</u>	9	HPV	E7	72	A
VQLDIQSTR	<u>681</u>	9	HPV	E7	72	A
SLGPGPGTK	<u>682</u>	9	Human	MAGE1	96	A
SLFGPGPGK	<u>683</u>	9	Human	MAGE1	96	A
LVGPGPGK	<u>684</u>	8	Human	MAGE2	116	A
KMFLQLAK	<u>685</u>	8	Human	p53	132	
KMGPGPGK	<u>686</u>	8	Human	p53	132	A
KQENWYSLKK	<u>687</u>	10	Pf	CSP	58	
GVGPGPGLK	<u>688</u>	9	Pf	LSA1	105	A
GVSHPGPGK	<u>689</u>	9	Pf	LSA1	105	A
FLLYILFLVK	<u>690</u>	10	Pf		17	
LVFSNVLCFR	<u>691</u>	10	Pf		43	
SSFDIKSEVK	<u>692</u>	10	Pf		116	
TLYQIQVMKR	<u>693</u>	10	Pf		44	
KQVQMMIMIK	<u>694</u>	10	Pf		58	
GVYIMIISK	<u>695</u>	10	Pf		70	
ELFDKDTFFK	<u>696</u>	10	Pf		158	
ALERLLSLKK	<u>697</u>	10	Pf		50	
KILIKIPVTK	<u>698</u>	10	Pf		109	
RLPLLPKTWK	<u>699</u>	10	Pf		128	
SQVSNSDSYK	<u>700</u>	10	Pf		161	
QQNQESKIMK	<u>701</u>	10	Pf		197	
IALLIIPPK	<u>702</u>	10	Pf		249	
SSPLFNIFYK	<u>703</u>	10	Pf		14	
FLYLLNKKNK	<u>704</u>	10	Pf		151	
LQMMNVNLQK	<u>705</u>	10	Pf		183	
LTNHLINTPK	<u>706</u>	10	Pf		195	
IFISFYLINK	<u>707</u>	10	Pf		259	
RLFEESLGIR	<u>708</u>	10	Pf		293	
LLYILFLVK	<u>709</u>	9	Pf		18	
KSMLKELIK	<u>710</u>	9	Pf		129	
PVLTSLFNK	<u>711</u>	9	Pf		166	
KTMNNYMIK	<u>712</u>	9	Pf		18	
LFDKDTFFK	<u>713</u>	9	Pf		159	
YLFNQHIKK	<u>714</u>	9	Pf		287	
MQSSFFMNR	<u>715</u>	9	Pf		307	
RFYITTRYK	<u>716</u>	9	Pf		315	
TTRYKYLNK	<u>717</u>	9	Pf		319	
AVIFTPIYY	<u>718</u>	9	Pf		34	
ALERLLSLK	<u>719</u>	9	Pf		50	
SISGKYDIK	<u>720</u>	9	Pf		85	
EQRLPLLPK	<u>721</u>	9	Pf		126	
IALLIIPPK	<u>722</u>	9	Pf		250	
PVCSMEYK	<u>723</u>	9	Pf		270	
VVCSMEYKK	<u>724</u>	9	Pf		271	
FSYDLRLNK	<u>725</u>	9	Pf		308	
HLNIPIGFK	<u>726</u>	9	Pf		323	

HLA-A3 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
PLFNNFYKR	<u>727</u>	9	Pf		16	
YQNFQNADK	<u>728</u>	9	Pf		141	
QMMNVNLQK	<u>729</u>	9	Pf		184	
AVSEIQNNK	<u>730</u>	9	Pf		222	
GTMYYLLKK	<u>731</u>	9	Pf		236	
FISFYLINK	<u>732</u>	9	Pf		260	
YLINKHWQR	<u>733</u>	9	Pf		264	
ALKISQLQK	<u>734</u>	9	Pf		273	
KINSNFLK	<u>735</u>	9	Pf		282	
AAMXDPTTFK	<u>736</u>	10	Unknown	Naturally processed		A
GTMITSXYK	<u>737</u>	9	Unknown	Naturally processed		A
SXXPAXFQK	<u>738</u>	9	Unknown	Naturally processed		A
ATAGDGXXEXRK	<u>739</u>	12	Unknown	Naturally processed		A

TABLE 16

HLA-A3 SUPERTYPE						
Sequence	SEQ ID	A*0301	A*1101	A*3101	A*3301	A*6801
	NO.					
ALNAAAAAK	<u>389</u>	74	21	10954	>72500	80000
ALAAGAAAK	<u>390</u>	19	37			
ALQAAAAAK	<u>391</u>	57	65	51962	>72500	>80000
STGPGPGVRR	<u>392</u>	18695	367	95	5983	5.8
STLPGPGVRR	<u>393</u>	892	19	42	670	3.8
STLPGPGGRR	<u>394</u>	297	19	61	1893	25
STLPEGPGGR	<u>395</u>	325	26	28	822	30
QAGFFLLTR	<u>396</u>	10138	1678	302	182	5.3
RVHFASPLH	<u>397</u>	12	60	572	>122881.36	7620
AAYAAQGYK	<u>398</u>	18	18	1175	14074	34
KSKFGYGAK	<u>399</u>	36	596	116	>122881.36	>7626.31
PAAYAAQGYK	<u>400</u>	950	456	20314	>110687.02	666
RMVVGVEH	<u>401</u>	3.8	274	162	>122881.36	>28776.98
SQLSAPSLK	<u>402</u>	306	25	1276	>122881.36	3845
TSCGNTLTCT	<u>403</u>	>36666.67	5.0			
VTGPGPGPVWK	<u>404</u>	2900	24	12964	>102836.88	425
VTVGPGPGVWK	<u>405</u>	174	2.7	2731	75360	21
VTVYGPBGWK	<u>406</u>	1151	18	>8995.5	>102836.88	206
VTVYGPBGPK	<u>407</u>	310	24	9720	101830	30
PVRPQVPLR	<u>408</u>	>10901.88	16112	332	3439	7012
HGAITSSNTK	<u>409</u>	2837	344	>16143.5	>22924.9	1235
AVDLSFFLK	<u>410</u>	226	23	6207	>27831.09	4038
DVSHFLKEK	<u>411</u>	>9298.39	5645	>17839.44	232	135
GVLDGLIYSK	<u>412</u>	1080	21	6007	>25151.78	831
GVDGLIYSK	<u>413</u>	10089	47	>17664.38	>29652.35	5100
EILDLWVYK	<u>414</u>	1032	64	>5774.78	288	93
ILDLWVYK	<u>415</u>	1265	320	13680	30096	12092
RVPLTFGWCFK	<u>416</u>	69	30	102	26651	571
QVYTPGPGTR	<u>417</u>	1249	852	1764	3334	273
AVGPGPGLK	<u>418</u>	18	3.6	128	75754	444
AVDGPBGPK	<u>419</u>	179	19	36837	>112403.1	2132
QMGPGPGNFK	<u>420</u>	49	22	2682	100771	63
QMAGPGPGFK	<u>421</u>	9.4	6.2	667	4784	30
QMAVGPGPGK	<u>422</u>	33	16	5961	86676	22
TVGPGPGPEK	<u>423</u>	115	17	10140	98177	23
TVQGPBGPEK	<u>424</u>	218	3.4	9874	103379	195
TVQGPBGPGK	<u>425</u>	41	2.5	1335	68584	28
VAIKIGGQLK	<u>426</u>	2593	151	46875	51222	123
VTVKIGGQLK	<u>427</u>	296	61	24385	104757	147
VTIKVGGQLK	<u>428</u>	188	59	6061	47647	127
VTIRIGGQLK	<u>429</u>	51	14	4458	65764	25
VTVRIGGQLK	<u>430</u>	226	15	5380	40344	49
VTVKVGGQLK	<u>431</u>	206	54	21484	46182	104
VTIRVGGQLK	<u>432</u>	43	13	3591	86086	28
VTVRVGGQLK	<u>433</u>	216	19	8238	>72319.2	141
VTVKIGGQLR	<u>434</u>	19185	194	417	3833	52

HLA-A3 SUPERTYPE						
Sequence	SEQ ID NO.	A*0301	A*1101	A*3101	A*3301	A*6801
VTIRIGGQLR	<u>435</u>	3192	23	61	1352	16
VTIKLGGQIR	<u>436</u>	43252	219	590	12965	104
VSIKVGQIK	<u>437</u>	1921	86	57069	>72319.2	2026
VSIRVGQIK	<u>438</u>	642	91	50677	>61702.13	1960
VTVKIEGQLK	<u>439</u>	647	23	4616	64604	30
VTIKIEGQLK	<u>440</u>	361	69	5077	58024	27
VTVKIEGQLR	<u>441</u>	35612	143	394	4057	146
VSIRVGQTK	<u>442</u>	341	21	29949	38958	290
VSIRVGQTR	<u>443</u>	18531	241	466	8595	288
VTVRIGGMQK	<u>444</u>	54	13	2583	44425	155
ITVKIGKEVR	<u>445</u>	>69182.39	12904	5057	24985	154
GTRQARRNK	<u>446</u>	67	749	9713	45966	59708
GTRQARRNRK	<u>447</u>	100	634	3800	>42335.77	7788
GTRQARRNRK	<u>448</u>	404	2596	7774	>24308.47	9104
GTRQTRKNK	<u>449</u>	198	3104	13373	>29713.11	18657
GTRQTRKNRK	<u>450</u>	129	1082	2485	60183	5998
GTRQTRKNRRK	<u>451</u>	478	4184	4008	>24308.47	>17167.38
RVRRRRWRAR	<u>452</u>	2443	>16759.78	265	3758	>36866.36
KVRRRRWRAR	<u>453</u>	327	>20905.92	342	3243	15501
LTISYGRK	<u>454</u>	988	708	27068	38162	482
KTLGISYGR	<u>455</u>	53	9.8	21	502	36
LTISYGRKK	<u>456</u>	584	69	13918	59654	63
GTSYGRKKR	<u>457</u>	9965	5916	225	21588	5778
GTGISYGRK	<u>458</u>	480	77	58102	>43740.57	7407
KTLGISYGRK	<u>459</u>	36	79	841	42378	1629
LTISYGRKKR	<u>460</u>	7161	1229	71	2515	33
KTLGISYGRKK	<u>461</u>	52	285	91	23401	647
TVCNNCYCK	<u>462</u>	9920	267	8793	28481	876
LVISYGRKKRR	<u>463</u>	>11702.13	8669	562	267	4662
ISYGRKKRRQK	<u>464</u>	48	2807	3147	>20000	4428
ETGPSGQCK	<u>465</u>	>14569.54	3501	>22500	>17813.27	50
KVGPGGYPRR	<u>466</u>	2268	487	250	7904	721
KAGPGGYPRK	<u>467</u>	62	43	10734	>17813.27	5555
KVGPGGYPRRK	<u>468</u>	70	87	775	>5063.73	921
AVPGGYPRR	<u>469</u>	3012	1215	1349	3453	109
AVPGGYPRRK	<u>470</u>	819	60	39974	>5570.5	846
KVGSLLQYLK	<u>471</u>	482	70	2104	>43740.57	4200
ETVRHFPR	<u>472</u>	>13513.51	4183	1000	81	86
AACHKCIDFY	<u>473</u>	18824	261	20643	>116465.86	32548
LLIRCLRCQK	<u>474</u>	437	170	6612	28936	78
KISEYRHYN	<u>475</u>	42	112	1426	35341	25077
AVCRVCLLFY	<u>476</u>	77	21	1978	4520	1302
FAFTDLTIVY	<u>477</u>	40343	21161	42065	131202	346
FAFADLTIVY	<u>478</u>	18592	5866	23676	26768	402
RFLSKISEYR	<u>479</u>	1640	18468	33	436	172
ILIRCIICQR	<u>480</u>	8550	5012	377	2480	537
RTAMFQDPQER	<u>481</u>	1478	103	49	3459	19
AMFQDPQERPR	<u>482</u>	1718	886	45	1787	1478

HLA-A3 SUPERTYPE						
Sequence	SEQ ID NO.	A*0301	A*1101	A*3101	A*3301	A*6801
MFQDPQERPRK	<u>483</u>	15493	8571	604	419	16729
DLLIRCINCQK	<u>484</u>	2923	935	4884	29	263
RFEDPTRRPYK	<u>485</u>	169	432	53	1758	7338
ELTEVFEFAPK	<u>486</u>	8966	582	25205	1733	15
GLYNLLIRCLR	<u>487</u>	1268	1568	250	401	1624
NLLIRCLRCQK	<u>488</u>	1565	854	3140	397	1480
EVLEESVHEIR	<u>489</u>	>45643.15	>20202.02	31037	212	240
EVYKFLFTDLR	<u>490</u>	31240	602	759	4.3	11
FLFTDLRIVYR	<u>491</u>	672	227	58	21	1.4
EVLEIPLIDLR	<u>492</u>	>47008.55	16638	36427	72	27
DLRLSCVYCKK	<u>493</u>	3644	1907	17023	109	3002
EVYNFACTELK	<u>494</u>	1622	117	484	5.9	2.7
RVCLLFYSKVR	<u>495</u>	771	190	221	1061	1267
LLFYSKVRKYR	<u>496</u>	28	94	7.0	11	15
QLCDLLIRCYR	<u>497</u>	1240	700	450	106	489
TLEQTVKK	<u>498</u>	4766	203	>100000	>75324.68	21400
ATRDLCIVYR	<u>499</u>	237	156	4.7	44	28
AFRDLCIVYK	<u>500</u>	31	15	10	132	57
ATCDKCLKFY	<u>501</u>	194	17	491	18080	4562
AVCDKCLKFR	<u>502</u>	77	15	11	45	34
KLYSKISEYR	<u>503</u>	5.4	168	6.4	28	91
KFYSKISEYK	<u>504</u>	7.6	674	27	329	208
KFSEYRHYCY	<u>505</u>	5092	7485	308	49397	14571
KISEYRHYCR	<u>506</u>	486	688	25	833	1488
LFIRCINCQK	<u>507</u>	2880	702	52	42	56
LLIRCINCQR	<u>508</u>	2818	686	30	50	14
KVRFHNIRGR	<u>509</u>	39	8632	27	4500	3979
KQRFHNIRGK	<u>510</u>	55	1953	573	35208	22879
WFGRCMSCCR	<u>511</u>	16071	10690	288	98	303
WTGRCMSCCK	<u>512</u>	6687	841	6496	15191	118
MTCCRSSRTR	<u>513</u>	3825	933	410	601	2.2
MSCRSSRTK	<u>514</u>	352	169	2333	6916	12
STCRSSRTRR	<u>515</u>	2989	118	152	1020	312
SCCRSSRTRK	<u>516</u>	326	3272	5592	20916	8777
DIEITCVYCR	<u>517</u>	2014	826	3780	448	422
FTFKDLFVVY	<u>518</u>	14364	1208	10757	2725	62
FAFKDLFVVK	<u>519</u>	783	71	525	1066	3.6
AVKDLFVVYR	<u>520</u>	1728	91	3.1	9.1	3.3
AFKDLFVVYK	<u>521</u>	3256	211	32	93	576
FVVYRDSIPK	<u>522</u>	265	81	6216	146	30
DTIPHAACHK	<u>523</u>	2366	701	1763	9.3	23
DSIPHAACHR	<u>524</u>	2772	853	357	2.2	27
KFIDFYSRIR	<u>525</u>	8891	9008	3.3	677	2551
DTVYGDTLEK	<u>526</u>	50	15	28754	55090	31
DSVYGDTLER	<u>527</u>	292	23	485	891	28
LFIRCLRCQK	<u>528</u>	3390	1533	218	77	200
LLIRCLRCQR	<u>529</u>	3360	1396	28	75	13
RVHNIAGHYR	<u>530</u>	30	21	22	114	18

HLA-A3 SUPERTYPE						
Sequence	SEQ ID	A*0301	A*1101	A*3101	A*3301	A*6801
	NO.					
RFHNIAGHYK	<u>531</u>	25	22	2.6	80	23
RTQCHSCCNR	<u>532</u>	338	20	22	132	161
RGQCHSCCNK	<u>533</u>	6135	113	425	37669	20340
ATDTLTIVYR	<u>534</u>	247	10	34	1739	14
AFTDLTIVYK	<u>535</u>	701	112	3952	9380	215
RLYSKVSEFR	<u>536</u>	6.4	131	24	690	73
RFYSKVSEFK	<u>537</u>	27	521	30	4452	547
KFSEFRWYRY	<u>538</u>	4750	1595	34	856	12811
KVSEFRWYRR	<u>539</u>	266	16	2.8	159	30
YFVYGTTLEK	<u>540</u>	204	62	2167	15740	53
YSVYGTTLER	<u>541</u>	430	96	2136	6903	19
GTTLEKLTNR	<u>542</u>	3604	1720	382	706	2946
LVIRCITCQR	<u>543</u>	2222	255	54	135	14
LLIRCITCQK	<u>544</u>	291	120	3009	2165	40
WVGRCIACWR	<u>545</u>	6227	1391	85	13	9.7
WTGRCIACWK	<u>546</u>	2633	55	3078	169	24
RTIACWRRPR	<u>547</u>	40	63	3.2	95	51
RCIACWRRPK	<u>548</u>	1535	1476	292	176	1655
AVADLTVVYR	<u>549</u>	489	11	31	892	7.3
AFADLTVVYK	<u>550</u>	2365	107	1113	13557	50
RVLSKISEYR	<u>551</u>	34	84	24	197	136
RFLSKISEYK	<u>552</u>	31	287	42	10237	112
KFSEYRHYNY	<u>553</u>	5819	5521	286	18351	1798
KISEYRHYNR	<u>554</u>	58	140	17	161	1579
ITIRCIICQR	<u>555</u>	488	93	50	123	12
ILIRCIICQK	<u>556</u>	192	78	1383	1423	165
WVGRCIACWR	<u>557</u>	2757	3973	360	24	19
WAGRCIACWK	<u>558</u>	4662	583	23311	1491	50
CFACWRSRRR	<u>559</u>	23542	7164	578	165	10206
DTSIACVYCK	<u>560</u>	2936	89	5385	1968	216
DVSIACVYCR	<u>561</u>	2814	217	406	487	658
CVYCKATLEK	<u>562</u>	418	653	5307	17928	862
RFEVYQFAFK	<u>563</u>	38	611	179	2867	2443
RTEVYQFAFR	<u>564</u>	217	78	12	142	147
AVKDL CIVYR	<u>565</u>	841	66	7.3	8.0	6.5
AFKDL CIVYK	<u>566</u>	856	47	39	263	378
ATCHKCIDFY	<u>567</u>	133	7.4	1164	12691	1386
AACHKCIDFK	<u>568</u>	118	20	437	53733	414
NLVYGETLEK	<u>569</u>	846	143	761	121	87
NSVYGETLER	<u>570</u>	150	25	163	1333	18
LSIRCLRCQK	<u>571</u>	245	14	100	1135	17
LLIRCLRCQY	<u>572</u>	727	452	2894	2430	254
RVHSIAGQYR	<u>573</u>	31	34	7.6	812	28
RFHSIAGQYK	<u>574</u>	17	43	1.3	629	83
LVTDLRIVYR	<u>575</u>	3869	648	20	150	6.8
LFTDLRIVYK	<u>576</u>	628	263	258	149	277
CTMCLRFLSK	<u>577</u>	1002	226	6274	3945	429
CIMCLRFLSR	<u>578</u>	41	101	167	83	155

HLA-A3 SUPERTYPE						
Sequence	SEQ ID	A*0301	A*1101	A*3101	A*3301	A*6801
	NO.					
RLLSKISEYR	<u>579</u>	5.2	662	7.7	108	21
RFLSKISEYY	<u>580</u>	1702	25535	14	41096	3999
SFYGKTLEER	<u>581</u>	642	205	17	66	42
SLYGKTLEEK	<u>582</u>	7.9	6.8	1044	6516	29
WFGRSECWR	<u>583</u>	1788	1569	20	5.5	26
WTGRSECWK	<u>584</u>	2492	26	3323	720	22
AFCRVCLLFY	<u>585</u>	509	272	1777	1202	173
AVCRVCLLFR	<u>586</u>	20	1.8	2.1	64	21
CFLFYSKVRK	<u>587</u>	125	96	81	315	172
CLLFYSKVRR	<u>588</u>	417	204	159	386	242
LVYSKVRKYR	<u>589</u>	320	619	17	49	31
LFYSKVRKYK	<u>590</u>	680	2582	18	30	1976
GTTLESITKK	<u>591</u>	622	108	85182	132509	10147
WVGSCCLGCWR	<u>592</u>	48682	5520	20	15	9.3
WTGSCCLGCWK	<u>593</u>	7705	6.9	18344	2980	3.7
VVADLRIVYR	<u>594</u>	513	18	41	101	16
VFADLRIVYK	<u>595</u>	2086	127	402	200	273
RTLSKISEYR	<u>596</u>	77	100	52	189	133
RLLSKISEYK	<u>597</u>	15	65	158	40019	429
KVSEYRHYNV	<u>598</u>	349	110	1791	70859	3498
KISEYRHYNK	<u>599</u>	29	18	397	24827	15565
IVIRCIICQR	<u>600</u>	984	217	52	529	28
WLGRCAVCWR	<u>601</u>	2330	3002	356	40	112
WTGRCAVCWK	<u>602</u>	1261	131	4176	3403	29
YVVCCKCLK	<u>603</u>	3282	643	8.5	165	1289
YAVCDKCLR	<u>604</u>	458	194	4261	26582	16034
SVCRSSRTR	<u>605</u>	323	97	249	547	17
SCCRSSRTK	<u>606</u>	21	3.9	51	5227	4.2
SLPHAACHK	<u>607</u>	32	66	219	1186	654
SIPHAACHR	<u>608</u>	1053	352	236	253	181
FVDLTIVYR	<u>609</u>	29674	5312	2384	430	138
FTDLTIVYK	<u>610</u>	557	16	24170	18477	143
SFYGTTLEK	<u>611</u>	34	15	517	3385	498
SVYGTTLER	<u>612</u>	28	6.4	133	454	21
TFLEKLTNK	<u>613</u>	6839	815	451	148	918
TTLEKLTNR	<u>614</u>	1993	817	42	37	101
ETNPFGICK	<u>615</u>	9585	100	29103	804	14
EGNPFGICR	<u>616</u>	11467	10372	5123	344	82
NTLEQTVKR	<u>617</u>	20380	1151	2273	18	8.6
ALCWRSSRR	<u>618</u>	959	9748	72	1289	7416
AACWRSSRK	<u>619</u>	75	770	3022	45341	12877
VSIACVYCR	<u>620</u>	3236	143	42	1347	185
SIACVYCKK	<u>621</u>	271	83	9114	19632	96
ILYRDCIAY	<u>622</u>	261	1832	53232	44670	>19607.84
IVYRDCIAR	<u>623</u>	465	106	27	325	64
CTAYAACHK	<u>624</u>	726	196	2956	771	167
CIAYAACHR	<u>625</u>	3625	1905	502	115	262
SFYGETLEK	<u>626</u>	288	108	947	885	1074

HLA-A3 SUPERTYPE						
Sequence	SEQ ID	A*0301	A*1101	A*3101	A*3301	A*6801
	NO.					
SVYGETLER	<u>627</u>	44	11	235	160	17
LIRCLRCQR	<u>628</u>	21335	12648	695	810	200
RTQCVQCKK	<u>629</u>	234	20	127	8147	3066
RLQCVQCKR	<u>630</u>	2535	6081	65	1829	11479
KFLEERVKK	<u>631</u>	5344	2229	30	9740	17674
KTLEERVKR	<u>632</u>	1957	159	37	1360	17685
NVMGRWTGR	<u>633</u>	3884	794	40	18	20
NIMGRWTGK	<u>634</u>	52	54	3274	86	173
LTYRDDFPY	<u>635</u>	8265	82	>71146.25	20186	1529
LVYRDDFPK	<u>636</u>	317	13	3009	1970	130
RFCLLFYSK	<u>637</u>	1156	484	83	450	232
RVCLLFYSR	<u>638</u>	439	111	51	2176	689
LTFYSKVRK	<u>639</u>	3.8	8.0	87	3382	13
LLFYSKVRR	<u>640</u>	56	73	38	276	11
ATLESITKR	<u>641</u>	1437	16	100	851	188
KVLCDLLIR	<u>642</u>	363	169	66	5896	9053
KQLCDLLIK	<u>643</u>	226	65	340	46426	11897
TFVHEIELK	<u>644</u>	4431	217	8412	4130	172
TSVHEIELR	<u>645</u>	>64327.49	872	1039	5948	12
YTFVFADLR	<u>646</u>	3633	8.1	20	6.6	2.9
DFLEQTLKK	<u>647</u>	>57591.62	18809	34365	174	14376
DTLEQTLKR	<u>648</u>	31347	12909	38127	9.2	110
LVRCHICQR	<u>649</u>	677	358	59	109	201
LIRCHICQK	<u>650</u>	445	252	639	834	285
RVAVCWRPR	<u>651</u>	5.3	8.5	7.0	102	33
RCAVCWRPK	<u>652</u>	285	340	382	131	1297
AFCWRPRRR	<u>653</u>	273	17907	60	75	1087
AVCWRPRRK	<u>654</u>	34	101	263	7950	1810
LSFVCPWCA	<u>655</u>	38337	10864	4289	4603	341
TFCKCDSTLR	<u>656</u>	21772	8043	332	91	260
LVVESSADDLR	<u>657</u>	>47008.55	2170	26410	5624	28
TLQVVCPCAR	<u>658</u>	20997	1395	67	63	147
YLIHVPCCECK	<u>659</u>	1748	1534	33044	8066	177
FVVQLDIQSTK	<u>660</u>	3682	853	48593	31350	2.7
HTCNTTVR	<u>661</u>	4862	1792	726	4490	25
GLVCPICSQK	<u>662</u>	428	814	45293	70317	3568
GFNHQHLPAR	<u>663</u>	>46610.17	27889	173	5572	34617
GVNHQHLPK	<u>664</u>	42	11	3337	76239	9347
NVVTFCQCK	<u>665</u>	790	303	4757	87	13
NIVTFCCQR	<u>666</u>	1507	1070	2731	766	93
GVSHAQLPAK	<u>667</u>	42	12	36011	>74935.4	20590
LIHVPCCECR	<u>668</u>	5326	5925	385	387	228
AVLQDIVLH	<u>669</u>	1922	101	6307	25776	27035
ATLQDIVLK	<u>670</u>	37	8.6	65	17121	3231
GVNHQHLPK	<u>671</u>	26	7.7	353	15615	1192
HVMLCMCKK	<u>672</u>	282	79	772	825	99
HTMLCMCCR	<u>673</u>	405	92	11	14	24
LSFVCPWCR	<u>674</u>	31676	200	47	231	152

HLA-A3 SUPERTYPE						
Sequence	SEQ ID NO.	A*0301	A*1101	A*3101	A*3301	A*6801
AQPATADYK	<u>675</u>	3500	109	10413	58871	24173
VVHAQLPAR	<u>676</u>	423	127	3.4	12	201
VSHAQLPAK	<u>677</u>	378	9.5	46	1401	13502
QLARQAKQH	<u>678</u>	8423	6862	945	1665	243
KQHTCYLIR	<u>679</u>	135	213	13	2275	12177
VTLDIQSTK	<u>680</u>	78	13	2046	1954	237
VQLDIQSTR	<u>681</u>	15105	2917	162	4588	10341
SLGPGPGTK	<u>682</u>	7.8	5.8	4392	152133	3517
SLFGPGPGK	<u>683</u>	3.4	2.3	1085	82275	36
LVGPGPGK	<u>684</u>	1004	291	23907	>125541.13	598
KMFLQLAK	<u>685</u>	45	62	677	>125541.13	8384
KMGPGPGK	<u>686</u>	84	242	1144	106362	4156
KQENWYSLKK	<u>687</u>	608	178	6327	>136150.23	4794
GVGPGPGLK	<u>688</u>	47	4.0	1367	>111538.46	3972
GVSGPGPGK	<u>689</u>	13	5.8	>11221.95	>111538.46	209
FLLYILFLVK	<u>690</u>	446	1431	54496	3254	2266
LVFSNVLCFR	<u>691</u>	120	19	33	19	7.7
SSFDIKSEVK	<u>692</u>	1900	19	19829	70344	31
TLYQIQVMKR	<u>693</u>	361	164	397	558	90
KQVQMMIMIK	<u>694</u>	264	112	4627	1231	2247
GVIYIMIISK	<u>695</u>	777	18	18811	1567	1134
ELFDKDTFFK	<u>696</u>	144	109	3676	13	3.6
ALERLLSLKK	<u>697</u>	147	822	33559	18255	22391
KILIKIPVTK	<u>698</u>	13	60	1661	24992	19571
RLPLLPKTWK	<u>699</u>	11	67	340	11392	2889
SQVNSDSYK	<u>700</u>	1656	83	24559	>17448.86	1384
QQNQESKIMK	<u>701</u>	3469	77	28120	>17448.86	21310
IALLIIPPK	<u>702</u>	30	5.3	23822	8426	82
SSPLFNNFYK	<u>703</u>	100	0.7	1608	1728	6.3
FLYLLNKKNK	<u>704</u>	177	475	4313	780	155
LQMMNVNLQK	<u>705</u>	25	7.2	435	1113	320
LTNHLINTPK	<u>706</u>	11	5.9	62	373	10
IFISFYLINK	<u>707</u>	1987	1056	462	394	363
RLFEEGLGIR	<u>708</u>	64	1096	297	788	409
LLYILFLVK	<u>709</u>	13	207	90687	13261	5545
KSMLEKELIK	<u>710</u>	189	151	450	>46548.96	>37037.04
PVLTSLFNK	<u>711</u>	1949	25	5107	18271	29928
KTMNNYMIK	<u>712</u>	17	5.5	24	12743	29
LFDKDTFFK	<u>713</u>	931	167	5706	1189	101
YLFNQHIKK	<u>714</u>	14	7.8	4919	7974	14
MQSSFFMNR	<u>715</u>	13	1.1	29	75	3.8
RFYITTRYK	<u>716</u>	1.9	67	15	98	17468
TTRYKYLNK	<u>717</u>	117	848	416	652	2565
AVIFTPIYY	<u>718</u>	25	9.5	42321	10068	1352
ALERLLSLK	<u>719</u>	233	369	3433	12786	13708
SISGKYDIK	<u>720</u>	2086	50	28249	12437	1745
EQRLPLLPK	<u>721</u>	1088	765	423	987	1911
IALLIIPPK	<u>722</u>	1241	108	2926	1404	1965

HLA-A3 SUPERTYPE						
Sequence	SEQ ID NO.	A*0301	A*1101	A*3101	A*3301	A*6801
PVVCSMEYK	<u>723</u>	1940	80	330791	22608	414
VVCSMEYKK	<u>724</u>	443	54	891	14328	167
FSYDLRLNK	<u>725</u>	29	4.9	461	1264	15
HLNIPIGFK	<u>726</u>	2.3	1.3	183	97	2.8
PLFNIFYKR	<u>727</u>	2635	1890	520	1258	132
YQNFQNADK	<u>728</u>	2712	177	44698	>18447.84	19830
QMMNVNLQK	<u>729</u>	20	7.0	504	6649	243
AVSEIQNNK	<u>730</u>	25	11	1429	25449	14
GTMYILLKK	<u>731</u>	2.2	1.2	29	8453	3.1
FISFYLINK	<u>732</u>	19	9.0	2192	1456	18
YLINKHWQR	<u>733</u>	1034	676	4.4	7.7	3.7
ALKISQLQK	<u>734</u>	15	96	3203	23800	>54794.52
KINSNFLK	<u>735</u>	17	6.4	68	47740	2737
AAMXDPTTFK	<u>736</u>	50	7.2			
GTMTTSXYK	<u>737</u>	4.0	4.5			
SXXPAXFQK	<u>738</u>	14	2.0			
ATAGDGXXEXRK	<u>739</u>	184	19			

TABLE 17

HLA-A24 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
AYGPGPGKF	<u>740</u>	9	Artificial sequence	Consensus		A
AYIGPGPGF	<u>741</u>	9	Artificial sequence	Consensus		A
AYAAAAAAL	<u>742</u>	9	Artificial sequence			Poly
AYSSWMYSY	<u>743</u>	9	EBV	EBNA3	176	
DLLDTASALY	<u>744</u>	10	HBV	Core	419	
WFHISCLTF	<u>745</u>	9	HBV	NUC	102	
KYTSFPWL	<u>746</u>	8	HBV	pol	745	
FAAPFTQCGY	<u>747</u>	10	HBV	pol	631	
SYQHFRKLLL	<u>748</u>	10	HBV	POL	4	
LYSHPIILGF	<u>749</u>	10	HBV	POL	492	
MSTTDLEAY	<u>750</u>	9	HBV	X	103	
MYVGDLGGSVF	<u>751</u>	11	HCV	E1	275	
MYGPGPGGSVF	<u>752</u>	11	HCV	E1	275	A
MYVGPGPGSVF	<u>753</u>	11	HCV	E1	275	A
MYVGGPGPGVF	<u>754</u>	11	HCV	E1	275	A
MYVGDPGPGPF	<u>755</u>	11	HCV	E1	275	A
VMGSSYGF	<u>756</u>	8	HCV	NS5	2639	
EVDGVR LHRY	<u>757</u>	10	HCV	NS5	2129	
KYSKSSIVGW	<u>758</u>	10	HIV	NEF	4	A
KWSKSSIVGF	<u>759</u>	10	HIV	NEF	4	A
FFLKEKGGF	<u>760</u>	9	HIV	NEF	116	A
IYSKKRQEF	<u>761</u>	9	HIV	NEF	175	A
IYSKKRQEIF	<u>762</u>	10	HIV	NEF	175	A
LYVYHTQGYF	<u>763</u>	10	HIV	NEF	190	A
VYHTQGYFPDF	<u>764</u>	11	HIV	NEF	192	A
RYPLTFGW	<u>765</u>	8	HIV	NEF	216	
RYPLTFGF	<u>766</u>	8	HIV	NEF	216	A
RFPLTFGF	<u>767</u>	8	HIV	NEF	216	A
TYGWCFKL	<u>768</u>	8	HIV	NEF	222	A
TFGWCFKF	<u>769</u>	8	HIV	NEF	222	A
LYVYHTQGY	<u>770</u>	9	HIV	NEF	190	A
NYTPGPGIRF	<u>771</u>	10	HIV	NEF	206	A
QYPPLERLTL	<u>772</u>	10	HIV	REV	78	A
QLPPLERLTF	<u>773</u>	10	HIV	REV	78	A
KYGSLQYLAL	<u>774</u>	10	HIV	VIF	146	A
LSKISEYRHY	<u>775</u>	10	HPV	E6	70	
ISEYRHYNY	<u>776</u>	9	HPV	E6	73	
RFHNIRGRW	<u>777</u>	9	HPV	E6	131	
RFLSKISEY	<u>778</u>	9	HPV	E6	68	
RFHNISGRW	<u>779</u>	9	HPV	E6	124	
VYDFAFRDLCI	<u>780</u>	11	HPV	E6	49	
PYAVCDKCLKF	<u>781</u>	11	HPV	E6	66	
QYNKPLCDLLI	<u>782</u>	11	HPV	E6	98	

HLA-A24 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
PFGICKLCLRF	<u>783</u>	11	HPV	E6	59	
VYQFAFKDLCI	<u>784</u>	11	HPV	E6	44	
AYAACHKCIDF	<u>785</u>	11	HPV	E6	61	
VYKFLFTDLRI	<u>786</u>	11	HPV	E6	42	
PYGVCIMCLRF	<u>787</u>	11	HPV	E6	59	
PYAVCRVCLLF	<u>788</u>	11	HPV	E6	62	
VYDFVFADLRI	<u>789</u>	11	HPV	E6	42	
QYNKPLCDLF	<u>790</u>	10	HPV	E6	98	A
VYEFAFKDLF	<u>791</u>	10	HPV	E6	44	A
FYSKVSEFRF	<u>792</u>	10	HPV	E6	69	A
VYREGNPFGE	<u>793</u>	10	HPV	E6	53	A
FYSRIRELRF	<u>794</u>	10	HPV	E6	71	A
PYAVCRVCLF	<u>795</u>	10	HPV	E6	62	A
FYSKVRKYRF	<u>796</u>	10	HPV	E6	72	A
LYGDTLEQTF	<u>797</u>	10	HPV	E6	83	A
VYDFAFRDF	<u>798</u>	9	HPV	E6	49	A
AYRDLICIVY	<u>799</u>	9	HPV	E6	53	A
AFRDLICIVF	<u>800</u>	9	HPV	E6	53	A
PYAVCDKCF	<u>801</u>	9	HPV	E6	66	A
KYYSKISEY	<u>802</u>	9	HPV	E6	75	A
KFYSKISEF	<u>803</u>	9	HPV	E6	75	A
CYSLYGTTF	<u>804</u>	9	HPV	E6	87	A
RYHNIRGRW	<u>805</u>	9	HPV	E6	131	A
RFHNIRGRF	<u>806</u>	9	HPV	E6	131	A
VYCKTVLEF	<u>807</u>	9	HPV	E6	33	A
AYKDLFVVY	<u>808</u>	9	HPV	E6	48	A
AFKDLFVVF	<u>809</u>	9	HPV	E6	48	A
LYVVYRDSI	<u>810</u>	9	HPV	E6	52	A
LFVVYRDSF	<u>811</u>	9	HPV	E6	52	A
RYHNIAGHY	<u>812</u>	9	HPV	E6	126	A
RFHNIAGHF	<u>813</u>	9	HPV	E6	126	A
VYGTTLKCF	<u>814</u>	9	HPV	E6	83	A
AYADLTVVY	<u>815</u>	9	HPV	E6	46	A
AFADLTVVF	<u>816</u>	9	HPV	E6	46	A
RYLSKISEY	<u>817</u>	9	HPV	E6	68	A
NYSVYGNTF	<u>818</u>	9	HPV	E6	80	A
RYHNISGRW	<u>819</u>	9	HPV	E6	124	A
AYKDLICIVY	<u>820</u>	9	HPV	E6	48	A
AFKDLICIVF	<u>821</u>	9	HPV	E6	48	A
AYAACHKCF	<u>822</u>	9	HPV	E6	61	A
VYGETLEKF	<u>823</u>	9	HPV	E6	85	A
RYHSIAGQY	<u>824</u>	9	HPV	E6	126	A
RFHSIAGQF	<u>825</u>	9	HPV	E6	126	A
KYLFTDLRI	<u>826</u>	9	HPV	E6	44	A
KFLFTDLRF	<u>827</u>	9	HPV	E6	44	A
LYTDLRIVY	<u>828</u>	9	HPV	E6	46	A
LFTDLRIVF	<u>829</u>	9	HPV	E6	46	A

HLA-A24 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
PYGVCIMCF	<u>830</u>	9	HPV	E6	59	A
RFLSKISEF	<u>831</u>	9	HPV	E6	68	A
EYRHYQYSF	<u>832</u>	9	HPV	E6	75	A
RYHNIMGRW	<u>833</u>	9	HPV	E6	124	A
RFHNIMGRF	<u>834</u>	9	HPV	E6	124	A
VYNFACTEF	<u>835</u>	9	HPV	E6	45	A
NYACTELKL	<u>836</u>	9	HPV	E6	47	A
NFACTELKF	<u>837</u>	9	HPV	E6	47	A
PYAVCRVCF	<u>838</u>	9	HPV	E6	62	A
LYYSKVRKY	<u>839</u>	9	HPV	E6	71	A
LFYSKVRKF	<u>840</u>	9	HPV	E6	71	A
VYDFVFADF	<u>841</u>	9	HPV	E6	42	A
VYADLRIVY	<u>842</u>	9	HPV	E6	46	A
VFADLRIVF	<u>843</u>	9	HPV	E6	46	A
NYSLYGDTF	<u>844</u>	9	HPV	E6	80	A
RFHNISGRF	<u>845</u>	9	HPV	E6	124	A
LYNLLIRCF	<u>846</u>	9	HPV	E6	98	A
FYSKVSEF	<u>847</u>	8	HPV	E6	69	
VYREGNPF	<u>848</u>	8	HPV	E6	53	
VFEFAFKDLF	<u>849</u>	10	HPV	E6	44	
EYRHYCYSLY	<u>850</u>	10	HPV	E6	82	
EYRHYNYSLY	<u>851</u>	10	HPV	E6	75	
ETRHYCYSLY	<u>852</u>	10	HPV	E6	82	A
EYDHYCYSLY	<u>853</u>	10	HPV	E6	82	A
KTRYDYSVY	<u>854</u>	10	HPV	E6	78	A
KYDYYDYSVY	<u>855</u>	10	HPV	E6	78	A
ETRHYNYSLY	<u>856</u>	10	HPV	E6	75	A
EYDHYNYSLY	<u>857</u>	10	HPV	E6	75	A
TYCCKCDSTL	<u>858</u>	10	HPV	E7	56	A
TFCKCDSTF	<u>859</u>	10	HPV	E7	56	A
TYCHSCDSTF	<u>860</u>	10	HPV	E7	58	A
CYTCTTVRF	<u>861</u>	10	HPV	E7	59	A
LYPEPTDLF	<u>862</u>	9	HPV	E7	15	A
NYYIVTCCF	<u>863</u>	9	HPV	E7	52	A
LFLNTLSF	<u>864</u>	8	HPV	E7	89	
LFLSTLSF	<u>865</u>	8	HPV	E7	90	
RVLPPNWKY	<u>866</u>	9	Human	40s ribo prot S13	132	
RLAHEVGWKY	<u>867</u>	10	Human	60s ribo prot L13A	139	
AYKKQFSQY	<u>868</u>	9	Human	60s ribo prot L5	217	
KTKDIVNGL	<u>869</u>	9	Human	Factin capping protein	235	
SLFVSNHAY	<u>870</u>	9	Human	fructose biphosphatealdolase	355	
TYGPGPGSLSF	<u>871</u>	11	Human	Her2/neu	63	A
TYLPGPGLSF	<u>872</u>	11	Human	Her2/neu	63	A
TYLPGPGPGSF	<u>873</u>	11	Human	Her2/neu	63	A
TYLPTGPGPGF	<u>874</u>	11	Human	Her2/neu	63	A
RWGLLLALL	<u>875</u>	9	Human	Her2/neu	8	

HLA-A24 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
PYVSRLGI	<u>876</u>	9	Human	Her2/neu	780	
TYLPTNASL	<u>877</u>	9	Human	Her2/neu	63	
IYGPGLIF	<u>878</u>	10	Human	MAGE3	195	A
IYPGPGGIF	<u>879</u>	10	Human	MAGE3	195	A
IYPKGPGPGF	<u>880</u>	10	Human	MAGE3	195	A
RISGVDRYY	<u>881</u>	9	Human	NADH ubiquinone reductase	53	
LYSACFWWL	<u>882</u>	9	Human	OA1	194	
LYSACFWWF	<u>883</u>	9	Human	OA1	194	A
TYSVSFDSL	<u>884</u>	10	Human	PSM	624	
TYGPGSLF	<u>885</u>	10	Human	PSM	624	A
TYSGPGSLF	<u>886</u>	10	Human	PSM	624	A
TYSGPGPGF	<u>887</u>	10	Human	PSM	624	A
AYPNVSAKI	<u>888</u>	9	Lysteria	listeriolysin	196	
AYGPGPGKI	<u>889</u>	9	Lysteria	listeriolysin	196	A
IMVLSFLF	<u>890</u>	8	Pf	CSP	427	
YYGKQENW	<u>891</u>	8	Pf	CSP	55	
VFNVNSSI	<u>892</u>	9	Pf	CSP	416	
ALFQEQCY	<u>893</u>	9	Pf	CSP	18	
LYNTEKGRHPF	<u>894</u>	11	Pf	EXP	100	
YFILVNLL	<u>895</u>	8	Pf	LSA	10	
KFFDKDKEL	<u>896</u>	9	Pf	LSA	76	
KFIKSLFHI	<u>897</u>	9	Pf	LSA	1876	
YFILVNLLIF	<u>898</u>	10	Pf	LSA	10	
FYFILVNLLIF	<u>899</u>	11	Pf	LSA	9	
SFYFILVNLLI	<u>900</u>	11	Pf	LSA	8	
VFLIFFDLF	<u>901</u>	9	Pf	SSP2	13	
LYLLMDCSGSI	<u>902</u>	11	Pf	SSP2	49	
KVSDEIWN	<u>903</u>	9	Pf		182	
SYKSSKRDKF	<u>904</u>	10	Pf		225	
RYQDPQNYEL	<u>905</u>	10	Pf		21	
DFFLKSKFNI	<u>906</u>	10	Pf		3	
IFHFFLFL	<u>907</u>	9	Pf		11	
VFLVFSNVL	<u>908</u>	9	Pf		41	
TYGIIVPVL	<u>909</u>	9	Pf		160	
NYMKIMNHL	<u>910</u>	9	Pf		34	
TYKKKNNHI	<u>911</u>	9	Pf		264	
VYYNILIVL	<u>912</u>	9	Pf		277	
LYYLFNQHI	<u>913</u>	9	Pf		285	
SFFMNRFYI	<u>914</u>	9	Pf		310	
FYITTRYKY	<u>915</u>	9	Pf		316	
KYINFINFI	<u>916</u>	9	Pf		328	
KYEALIKLL	<u>917</u>	9	Pf		380	
IYYFDGNSW	<u>918</u>	9	Pf		40	
VYRHCEYIL	<u>919</u>	9	Pf		94	
TWKPTIFLL	<u>920</u>	9	Pf		135	
SYKVNCINF	<u>921</u>	9	Pf		168	

HLA-A24 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
KYNYFIHFF	<u>922</u>	9	Pf		216	
NYFIHFFTW	<u>923</u>	9	Pf		218	
HFFTWGTMF	<u>924</u>	9	Pf		222	
MFVPKYFEL	<u>925</u>	9	Pf		229	
IYTHIQDQL	<u>926</u>	9	Pf		295	
FFLKSKFNI	<u>927</u>	9	Pf		4	
RMTSLKNEI	<u>928</u>	9	Pf		61	
YYNNFNNNY	<u>929</u>	9	Pf		77	
YYNKSTEKL	<u>930</u>	9	Pf		87	
EYEPTANLL	<u>931</u>	9	Pf		109	
VYXKHPVSX	<u>932</u>	9	Unknown	Naturally processed		A
TYGNXTVTV	<u>933</u>	9	Unknown	Naturally processed		A
KYPDRVVPX	<u>934</u>	9	Unknown	Naturally processed		A
VYVXSXVTX	<u>935</u>	9	Unknown	Naturally processed		A
DAQXXXNTX	<u>936</u>	9	Unknown	Naturally processed		A
KYQAVTTTL	<u>937</u>	9	Unknown	Tumor p198	197	
KYGP GPGTTTL	<u>938</u>	11	Unknown	Tumor p198	197	A
KYQGP GPGTTTL	<u>939</u>	11	Unknown	Tumor p198	197	A

TABLE 18

HLA-A24 SUPERTYPE					
Sequence	SEQ ID NO.	A*2402	A*2301	A*2902	A*3002
AYGPGPGKF	<u>740</u>	2.4	9.7	44854	3.2
AYIGPGPGF	<u>741</u>	217	12	15887	5728
AYAAAAAAL	<u>742</u>	443			
AYSSWMYSY	<u>743</u>		21		4.9
DLLDTASALY	<u>744</u>			74	37
WFHISCLTF	<u>745</u>	204	11	95	75094
KYTSFPWL	<u>746</u>	208	177	>172413.79	346
FAAPFTQCGY	<u>747</u>			461	1364
SYQHFRKLLL	<u>748</u>	418	39	28	3768
LYSHPIILGF	<u>749</u>	2.6	5.4	109	1116
MSTTDLEAY	<u>750</u>			2565	396
MYVGDLCGSVF	<u>751</u>	26	0.91	612	1460
MYGPGPGGSVF	<u>752</u>	35	5.4	48442	31980
MYVGPGPGSVF	<u>753</u>	35	4.4	1527	28177
MYVGPGPGGVF	<u>754</u>	381	85	89	2870
MYVGDPGPGF	<u>755</u>	90	11	8656	39608
VMGSSYGF	<u>756</u>	36	159	145	41967
EVDGVRLHRY	<u>757</u>			14940	113
KYSKSSIVGW	<u>758</u>	4061	491	>69444.44	>34482.76
KWSKSSIVGF	<u>759</u>	1674	84	>56179.78	30367
FFLKEKGGF	<u>760</u>	3456	655	3015	141
IYSKKRQEF	<u>761</u>	306	421	29353	727
IYSKKRQEIF	<u>762</u>	238	360	>131578.95	21001
LYVYHTQGYF	<u>763</u>	38	23	1696	1222
VYHTQGYFPDF	<u>764</u>	149	68	14923	>22556.39
RYPLTFGW	<u>765</u>	127	3836	13889	6251
RYPLTFGF	<u>766</u>	3.3	6.4	9704	6328
RFPLTFGF	<u>767</u>	178	124	12759	13472
TYGWCFKL	<u>768</u>	2181	333	25658	>8042.9
TFGWCFKF	<u>769</u>	3424	462	4449	>10135.14
LYVYHTQGY	<u>770</u>	7140	6088	216	258
NYTPGPGIRF	<u>771</u>	483	37	8334	>9646.3
QYPPLERLTL	<u>772</u>	211	22	>11520.74	>9646.3
QLPPLERLTF	<u>773</u>	2507	338	>37313.43	>36585.37
KYGSLLQYLAL	<u>774</u>	2800	147	>69444.44	6957
LSKISEYRHY	<u>775</u>	>93023.26	>23671.5	55190	186
ISEYRHYNY	<u>776</u>	125794	>23557.69	1329	32
RFHNIRGRW	<u>777</u>	53237	11416	18	58
RFLSKISEY	<u>778</u>	472	121	34623	23
RFHNISGRW	<u>779</u>	>80536.91	22871	174	37
VYDFAFRDLCI	<u>780</u>	44	8.9	62242	35724
PYAVCDKCLKF	<u>781</u>	99	8.1	118249	>60000
QYNKPLCDLLI	<u>782</u>	303	36	>166666.67	6680

HLA-A24 SUPERTYPE					
Sequence	SEQ ID NO.	A*2402	A*2301	A*2902	A*3002
PFGICKLCLRF	<u>783</u>	137	19	1249	32803
VYQFAFKDLCI	<u>784</u>	30	1.9	49276	3477
AYAACHKCIDF	<u>785</u>	91	14	1264	4699
VYKFLFTDLRI	<u>786</u>	37	14	30216	1865
PYGVCIMCLRF	<u>787</u>	380	100	69	43722
PYAVCRVCLLF	<u>788</u>	226	150	2711	53351
VYDFVFADLRI	<u>789</u>	47	8.0	8904	7585
QYNKPLCDLF	<u>790</u>	115	21	7658	525
VYEF AFKDLF	<u>791</u>	15	1.7	1973	2038
FYSKVSEFRF	<u>792</u>	7.1	2.2	79	18453
VYREGNPF GF	<u>793</u>	197	91	11120	21947
FYSRIRE LRF	<u>794</u>	11	1.6	83	12598
PYAVCRVCLF	<u>795</u>	12	4.5	407	5226
FYSKVRKYRF	<u>796</u>	18	13	3042	1232
LYGDTLEQTF	<u>797</u>	91	24	40871	42025
VYDFAFRDF	<u>798</u>	9.6	19	47381	8490
AYRDL CIVY	<u>799</u>	2094	1479	7117	66
AFRDL CIVF	<u>800</u>	1005	369	6722	3305
PYAVCDKCF	<u>801</u>	216	183	122025	9884
KYYSKISEY	<u>802</u>	10951	2165	702	1.3
KFYSKISEF	<u>803</u>	174	138	73339	306
CYSLYGTTF	<u>804</u>	28	11	2088	7823
RYHNIRGRW	<u>805</u>	145	14	122644	15
RFHNIRGRF	<u>806</u>	29	2.4	346	0.69
VYCKTVLEF	<u>807</u>	50	4.7	610	1139
AYKDLFVVY	<u>808</u>	1549	905	639	1.3
AFKDLFVVF	<u>809</u>	294	6.8	3051	829
LYVVYRDSI	<u>810</u>	982	242	148359	3483
LFVVYRDSF	<u>811</u>	268	134	919	18
RYHNIAGHY	<u>812</u>	1227	195	138	0.93
RFHNIAGHF	<u>813</u>	37	17	635	1.4
VYGT TLEKF	<u>814</u>	19	13	75267	220
AYADLT VVY	<u>815</u>	369	1384	136	9.3
AFADLT VVF	<u>816</u>	203	30	779	137
RYLSKISEY	<u>817</u>	142	98	4247	1.1
NYSVYGNTF	<u>818</u>	28	29	9121	2559
RYHNISGRW	<u>819</u>	47	15	104884	13
AYKDL CIVY	<u>820</u>	33798	3036	5205	29
AFKDL CIVF	<u>821</u>	284	16	5846	2305
AYAACHKCF	<u>822</u>	200	159	10972	3393
VYGETLEKF	<u>823</u>	45	14	91902	20009
RYHSIAGQY	<u>824</u>	3170	1904	544	1.4
RFHSIAGQF	<u>825</u>	28	2.9	481	1.2
KYLFTDLRI	<u>826</u>	108	1.9	78575	339
KFLFTDLRF	<u>827</u>	12	0.74	44	152
LYTDLRIVY	<u>828</u>	1986	1216	4.8	2.1

HLA-A24 SUPERTYPE					
Sequence	SEQ ID NO.	A*2402	A*2301	A*2902	A*3002
LFTDLRIVF	<u>829</u>	169	2.6	164	2649
PYGVCIMCF	<u>830</u>	190	147	144402	38850
RFLSKISEF	<u>831</u>	58	2.5	40103	201
EYRHYQYSF	<u>832</u>	21	2.3	13707	430
RYHNIMGRW	<u>833</u>	29	12	106990	7.1
RFHNIMGRF	<u>834</u>	39	2.6	174	1.3
VYNFACTEF	<u>835</u>	14	2.1	774	784
NYACTELKL	<u>836</u>	1741	131	77844	49107
NFACTELKF	<u>837</u>	211	13	46	6826
PYAVCRVCF	<u>838</u>	429	257	5602	316
LYYSKVRKY	<u>839</u>	21942	2735	1452	28
LFYSKVRKF	<u>840</u>	2008	277	11172	632
VYDFVFADF	<u>841</u>	9.9	2.2	1230	3961
VYADLRIVY	<u>842</u>	28	122	8.2	8.3
VFADLRIVF	<u>843</u>	23	2.5	87	24062
NYSLYGDTF	<u>844</u>	6.4	142	20945	64
RFHNISGRF	<u>845</u>	34	5.5	572	2.8
LYNLLIRCF	<u>846</u>	47	15	17958	2255
FYSKVSEF	<u>847</u>	21	18	3774	66667
VYREGNPF	<u>848</u>	554	147	10001	65970
VFEFAFKDLF	<u>849</u>	400			
EYRHYCYSLY	<u>850</u>			198	3.7
EYRHYNYSLY	<u>851</u>			956	12
ETRHYCYSLY	<u>852</u>			755	10
EYDHYCYSLY	<u>853</u>			799	77
KTRYDYSVY	<u>854</u>			87841	0.71
KYDYYDYSVY	<u>855</u>			5749	11
ETRHYNYSLY	<u>856</u>			5464	29
EYDHYNYSLY	<u>857</u>			777	93
TYCCKCDSTL	<u>858</u>	206	30	145803	16588
TFCKCDSTF	<u>859</u>	25	14	501	1167
TYCHSCDSTF	<u>860</u>	14	2.9	5236	3580
CYTCGTTVRF	<u>861</u>	41	18	7744	38331
LYPEPTDLF	<u>862</u>	38	17	1150	30732
NYIIVTCCF	<u>863</u>	27	12	2675	8398
LFLNTLSF	<u>864</u>	587	104	1013	118217
LFLSTLSF	<u>865</u>	2283	160	1034	>75000
RVLPPNWKY	<u>866</u>		>49000		3.0
RLAHEVGWKY	<u>867</u>		4631		3.8
AYKKQFSQY	<u>868</u>		10669		5.3
KTKDIVNGL	<u>869</u>		>49000		164
SLFVSNHAY	<u>870</u>		30295		1.1
TYGPGPGSLSF	<u>871</u>	7.1	1.7	9853	47246
TYLGPGLSLF	<u>872</u>	23	0.65	600	26889
TYLPGPGPSF	<u>873</u>	8.8	2.2	56183	7275
TYLPTGPGPGF	<u>874</u>	39	8.6	56574	32985

HLA-A24 SUPERTYPE					
Sequence	SEQ ID NO.	A*2402	A*2301	A*2902	A*3002
RWGLLLALL	<u>875</u>	106	100	61253	300
PYVSRLGI	<u>876</u>	11	18	200160	65465
TYLPTNASL	<u>877</u>	141	7.8	106153	8244
IYGPGLIF	<u>878</u>	7.4	8.0	58	6845
IYPGPGGIF	<u>879</u>	58	12	18659	17959
IYPKGPGPGF	<u>880</u>	7.5	4.9	53603	61283
RISGVDRYY	<u>881</u>		>49000		3.0
LYSACFWWL	<u>882</u>	28			
LYSACFWWF	<u>883</u>	28			
TYSVSFDSL	<u>884</u>	10	12	521	5218
TYGPGGSLF	<u>885</u>	3.9	8.7	7228	10871
TYSGGPGLF	<u>886</u>	50	92	7726	3461
TYSVGPGPGF	<u>887</u>	332	340	120913	55200
AYPNVSAKI	<u>888</u>	14	45	56905	4456
AYGPGPGKI	<u>889</u>	36	169	>156250	5427
IMVLSFLF	<u>890</u>	469	7.5	111	30000
YYGKQENW	<u>891</u>	85	951	>50000	>30000
VFNVVNSSI	<u>892</u>	403	35	24001	15737
ALFQEYQCY	<u>893</u>			149	1032
LYNTEKGRHPF	<u>894</u>	175	1947	>50000	>30000
YFILVNLL	<u>895</u>	96	82	4050	30000
KFFDKDKEL	<u>896</u>	269	>49000	>50000	3012
KFIKSLFHI	<u>897</u>	4.1	2.0	>50000	3495
YFILVNLLIF	<u>898</u>	577	12	764	3388
FYFILVNLLIF	<u>899</u>	599	50	902	9826
SFYFILVNLLI	<u>900</u>	229	35	3066	2096
VFLIFFDLF	<u>901</u>	40	12	1510	13554
LYLLMDCSGSI	<u>902</u>	154	10	5893	1469
KVSDEIWN	<u>903</u>	52169	>11980.44	230	1.9
SYKSSKRDKF	<u>904</u>	256	797	12594	88
RYQDPQNYEL	<u>905</u>	212	124	79717	189
DFFLKSKFNI	<u>906</u>	1648	304	47714	491
IFHFFLL	<u>907</u>	208	80	1405	837
VFLVFSNVL	<u>908</u>	26	4.9	33675	37689
TYGIIVPVL	<u>909</u>	248	20	30056	1519
NYMKIMNHL	<u>910</u>	16	1.7	45443	110
TYKKKNNHI	<u>911</u>	30	81	21642	162
VYYNILIVL	<u>912</u>	265	52	>192307.69	1127
LYYLFNQHI	<u>913</u>	33	1.4	20130	11035
SFFMNRFYI	<u>914</u>	172	11	200	1022
FYITTRYKY	<u>915</u>	350	11	9.6	7.5
KYINFINFI	<u>916</u>	11	0.72	25475	55
KYEALIKLL	<u>917</u>	2856	484	17296	16098
IYYFDGNSW	<u>918</u>	80	6.1	3101	3025
VYRHCEYIL	<u>919</u>	2200	64	117851	3326
TWKPTIFLL	<u>920</u>	148	11	21155	306

HLA-A24 SUPERTYPE					
Sequence	<u>SEQ</u> <u>ID</u> <u>NO.</u>	A*2402	A*2301	A*2902	A*3002
SYKVNCINF	<u>921</u>	27	15	2535	572
KYNYFIHFF	<u>922</u>	2.5	0.49	319	2.7
NYFIHFFTW	<u>923</u>	9.3	1.3	9774	3020
HFFTWGTMF	<u>924</u>	83	5.7	4.0	220
MFVPKYFEL	<u>925</u>	266	11	2560	8560
IYTHIQDQL	<u>926</u>	72	45	>37313.43	14124
FFLKSKFNI	<u>927</u>	1434	49	43105	>83333.33
RMTSLKNEL	<u>928</u>	12711	1807	40270	14
YYNNFNNNY	<u>929</u>	817	126	19	34
YYNKSTEKL	<u>930</u>	109	106	55636	21751
EYEPTANLL	<u>931</u>	127	44	>37313.43	>26086.96
VYXKHPVSX	<u>932</u>	4.3			
TYGNXTVTV	<u>933</u>	26			
KYPDRVVPX	<u>934</u>	224			
VYVXSXVTX	<u>935</u>	5.3			
DAQXXXNTX	<u>936</u>	5.9			
KYQAVTTTL	<u>937</u>	22	16	>156250	625
KYGP GPGTTTL	<u>938</u>	103	130	9180	7056
KYQGPGPGTTTL	<u>939</u>	543	438	74453	5999

TABLE 19

HLA-B7 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
APGPGPGLL		9	Artificial	Consensus		A
	<u>940</u>		sequence			
APRGPGPGL		9	Artificial	Consensus		A
	<u>941</u>		sequence			
QPRAPIRPI	<u>942</u>	9	EBNA		881	
YPLHEQHGM	<u>943</u>	9	EBNA		458	
CPTVQASKL	<u>944</u>	9	HBV	NUC	14	
SPTYKAFL	<u>945</u>	8	HBV	pol	659	
SPGPGPGL	<u>946</u>	8	HBV	pol	659	A
TPAGPGGVF	<u>947</u>	10	HBV	pol	354	A
TPARGPGPGF	<u>948</u>	10	HBV	pol	354	A
TPTGWGLAI	<u>949</u>	9	HBV	POL	691	
APCNFF TSA	<u>950</u>	9	HBV	X	146	
GPGHKARVI	<u>951</u>	9	HIV	GAG	390	A
RPQVPLRPM TI	<u>952</u>	11	HIV	NEF	98	A
FPVRPQVPI	<u>953</u>	9	HIV	NEF	94	A
RPQVPLRPI	<u>954</u>	9	HIV	NEF	98	A
RPQVPLRPM TI	<u>955</u>	11	HIV	NEF	98	A
YPLTFGWCI	<u>956</u>	9	HIV	NEF	217	A
FPLTFGWCI	<u>957</u>	9	HIV	NEF	217	A
FPLTFGWCFKI	<u>958</u>	11	HIV	NEF	217	A
FPVRPQVPL	<u>959</u>	9	HIV	nef	94	
FPGPGPGL	<u>960</u>	9	HIV	nef	94	A
FPVGPGL	<u>961</u>	9	HIV	nef	94	A
GPKVKQWPI	<u>962</u>	9	HIV	POL	197	A
LPPLERLTI	<u>963</u>	9	HIV	REV	79	A
CPEEKQRHL	<u>964</u>	9	HPV	E6	118	
VPGPGPGL	<u>965</u>	8	Human	Her2/neu	884	A
RPGPGGVSEF	<u>966</u>	11	Human	Her2/neu	966	A
RPRGPGGSEF	<u>967</u>	11	Human	Her2/neu	966	A
RPRFGPGGEF	<u>968</u>	11	Human	Her2/neu	966	A
RPRFRGPGGF	<u>969</u>	11	Human	Her2/neu	966	A
APGPGGAAPA	<u>970</u>	11	Human	p53	76	A
APAGPGGAPA	<u>971</u>	11	Human	p53	76	A
APAAGPGGPA	<u>972</u>	11	Human	p53	76	A
APAAPGGPGA	<u>973</u>	11	Human	p53	76	A
RPRGDNFAV	<u>974</u>	9	Pf	SSP2	305	
RPGPGGAV	<u>975</u>	9	Pf	SSP2	305	A
RPRGPGGV	<u>976</u>	9	Pf	SSP2	305	A
APRTVALTAL	<u>977</u>	10	Unknown	Naturally procesed		
APGPGGTAL	<u>978</u>	10	Unknown	Naturally procesed		A
APRGPGGAL	<u>979</u>	10	Unknown	Naturally procesed		A
APRTGPGPGL	<u>980</u>	10	Unknown	Naturally procesed		A
XVXD NATEY	<u>981</u>	9	Unknown	Naturally procesed		A
LGFVFTLTV	<u>982</u>	9	unknown			

TABLE 20

HLA-B*7 SUPERTYPE						
Sequence	SEQ ID NO.	B*0702	B*3501	B*5101	B*5301	B*5401
APGPGPGLL	<u>940</u>	299	7481	1614	18117	15613
APRGPGPGL	<u>941</u>	4.9	974	633	19779	1120
QPRAPIRPI	<u>942</u>	6770	>72000	>55000	12	>100000
YPLHEQHGM	<u>943</u>	>55000	20785	>55000	10	>100000
CPTVQASKL	<u>944</u>	3247	645	448	1861	21643
SPTYKAFL	<u>945</u>	109	31169	4665	54879	58651
SPGPGPGGL	<u>946</u>	173	2337	3535	25607	53272
TPAGPGPGVF	<u>947</u>	334	374	296	2629	351
TPARGPGPGF	<u>948</u>	144	1678	2418	2742	31768
TPTGWGLAI	<u>949</u>	76	5145	103	1343	172
APCNFF TSA	<u>950</u>	43	8087	1045	>22409.64	0.61
GPGHKARVI	<u>951</u>	1686	>72000	>55000	2.2	>50000
RPQVPLRPMTI	<u>952</u>	47009	>18997.36	8081	21518	129
FPVRPQVPI	<u>953</u>	94	124	39	222	9.1
RPQVPLRPI	<u>954</u>	367	>23225.81	>9001.64	85335	1215
RPQVPLRPMTI	<u>955</u>	140	10455	5045	21538	>15128.59
YPLTFGWCI	<u>956</u>	54283	1378	153	154	79
FPLTFGWCI	<u>957</u>	47951	164	63	36	14
FPLTFGWCFKI	<u>958</u>	52567	4991	590	188	105
FPVRPQVPL	<u>959</u>	17	3.8	18	49	21
FPGPGPGPL	<u>960</u>	1584	426	2330	21036	29900
FPVGPGL	<u>961</u>	106	14	138	32	246
GPKVKQWPI	<u>962</u>	5500	>72000	>55000	2.3	>50000
LPPLERLTI	<u>963</u>	24398	13399	359	2624	11243
CPEEKQRHL	<u>964</u>	10	>52554.74	>35483.87	>109411.76	>76923.08
VPGPGPGL	<u>965</u>	1517	447	537	4094	46405
RPGPGPGVSEF	<u>966</u>	119	18115	16774	20988	3360
RPRGPGPGSEF	<u>967</u>	11	24871	>14824.8	19336	2745
RPRFGPGPGEF	<u>968</u>	14	>30901.29	>14824.8	76844	15470
RPRFRGPGPGF	<u>969</u>	9.7	>30901.29	>14824.8	49682	60095
APGPGPGAAP		1112	1252	1317	4366	361
A	<u>970</u>					
APAGPGPGAP		161	>28915.66	11947	>39743.59	43
A	<u>971</u>					
APAAGPGPGP		173	12845	12470	28574	204
A	<u>972</u>					
APAAPGPGPG		811	3484	15814	>39240.51	158
A	<u>973</u>					
RPRGDNFAV	<u>974</u>	12	20386	1681	>46268.66	212
RPGPGPGAV	<u>975</u>	23	48487	2899	>46268.66	1891
RPRGPGPGV	<u>976</u>	11	2368	52	34831	47
APRTVALTAL	<u>977</u>	12	4351	14601	61596	16804
APGPGPGTAL	<u>978</u>	81	16315	16462	>43661.97	35965
APRGPGPGAL	<u>979</u>	11	23381	12732	>43661.97	1665
APRTGPGPGL	<u>980</u>	15	1414	1559	22012	2043
XVXDNATEY	<u>981</u>	>55000	444			>100000
LGFVFTLTV	<u>982</u>	849	>72000	27500	>93000	464

TABLE 21

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
SEAAAYAKKI	<u>983</u>	9	Artificial sequence	pool consensus		A
GEFPYKAAA	<u>984</u>	9	Artificial sequence	pool consensus		A
SEAPYKAIL	<u>985</u>	9	Artificial sequence	pool consensus		A
SEAPKYAIL	<u>986</u>	9	Artificial sequence	pool consensus		A
AEFKYIAAV	<u>987</u>	9	Artificial sequence	pool consensus		A
AEIPYLAKY	<u>988</u>	9	Artificial sequence	pool consensus		A
AEIPKLAYF	<u>989</u>	9	Artificial sequence	pool consensus		A
FPPDYAAAF	<u>990</u>	9	Artificial sequence			A
FPFKYKAAF	<u>991</u>	9	Artificial sequence			A
FPFKYAKAF	<u>992</u>	9	Artificial sequence			A
FPFKYAAAF	<u>993</u>	9	Artificial sequence			A
FAFKYAAAF	<u>994</u>	9	Artificial sequence			A
FQFKYAAAF	<u>995</u>	9	Artificial sequence			A
FDFKYAAAF	<u>996</u>	9	Artificial sequence			A
SENDRYRLL	<u>997</u>	9	EBV	BZLF1	209	A
IEDPPYNSL	<u>998</u>	9	EBV	Imp2	200	A
YEANGNLI	<u>999</u>	8	Flu	HA	259	A
YEDLRVLSF	<u>1000</u>	9	Flu	NP	338	A
SDYEGRLI	<u>1001</u>	8	Flu	NP	50	
GEISPYPSL	<u>1002</u>	9	Flu	NS1	158	A
MDIDPYKEF	<u>1003</u>	9	HBV	NUC	30	
LDKGIKPY	<u>1004</u>	8	HBV	POL	125	
ADLMGYIPL	<u>1005</u>	9	HCV	core	131	
LDPYARVAI	<u>1006</u>	9	HCV	NS5b	2663	A
AENLWVTVY	<u>1007</u>	9	HIV	gp120	1	
KENLWVTVY	<u>1008</u>	9	HIV	gp120	1	A
AEKLWVTVY	<u>1009</u>	9	HIV	gp120	1	A
AENKWVTVY	<u>1010</u>	9	HIV	gp120	1	A
AENLKVTVY	<u>1011</u>	9	HIV	gp120	1	A
AENLWKTVY	<u>1012</u>	9	HIV	gp120	1	A
AENLWVKVY	<u>1013</u>	9	HIV	gp120	1	A
AENLWVTKY	<u>1014</u>	9	HIV	gp120	1	A
AENLWVTVK	<u>1015</u>	9	HIV	gp120	1	A
FENLWVTVY	<u>1016</u>	9	HIV	gp120	1	A
VENLWVTVY	<u>1017</u>	9	HIV	gp120	1	A
PENLWVTVY	<u>1018</u>	9	HIV	gp120	1	A
NENLWVTVY	<u>1019</u>	9	HIV	gp120	1	A
DENLWVTVY	<u>1020</u>	9	HIV	gp120	1	A

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
TENLWVTVY	<u>1021</u>	9	HIV	gp120	1	A
YENLWVTVY	<u>1022</u>	9	HIV	gp120	1	A
ATNLWVTVY	<u>1023</u>	9	HIV	gp120	1	A
AEFLWVTVY	<u>1024</u>	9	HIV	gp120	1	A
AEVLWVTVY	<u>1025</u>	9	HIV	gp120	1	A
AEPLWVTVY	<u>1026</u>	9	HIV	gp120	1	A
AEDLWVTVY	<u>1027</u>	9	HIV	gp120	1	A
AENLWVTVY	<u>1028</u>	9	HIV	gp120	1	
AETLWVTVY	<u>1029</u>	9	HIV	gp120	1	A
AENFWVTVY	<u>1030</u>	9	HIV	gp120	1	A
AENVWVTVY	<u>1031</u>	9	HIV	gp120	1	A
AENPWVTVY	<u>1032</u>	9	HIV	gp120	1	A
AENDWVTVY	<u>1033</u>	9	HIV	gp120	1	A
AENNWVTVY	<u>1034</u>	9	HIV	gp120	1	A
AENTWVTVY	<u>1035</u>	9	HIV	gp120	1	A
AENLFVTVY	<u>1036</u>	9	HIV	gp120	1	A
AENLVVTVY	<u>1037</u>	9	HIV	gp120	1	A
AENLPVTVY	<u>1038</u>	9	HIV	gp120	1	A
AENLDVTVY	<u>1039</u>	9	HIV	gp120	1	A
AENLNVTVY	<u>1040</u>	9	HIV	gp120	1	A
AENLTVTVY	<u>1041</u>	9	HIV	gp120	1	A
AENLWFTVY	<u>1042</u>	9	HIV	gp120	1	A
AENLWLTVY	<u>1043</u>	9	HIV	gp120	1	A
AENLWPTVY	<u>1044</u>	9	HIV	gp120	1	A
AENLWDTVY	<u>1045</u>	9	HIV	gp120	1	A
AENLWNTVY	<u>1046</u>	9	HIV	gp120	1	A
AENLWTTVY	<u>1047</u>	9	HIV	gp120	1	A
AENLWVIFY	<u>1048</u>	9	HIV	gp120	1	A
AENLWVVVY	<u>1049</u>	9	HIV	gp120	1	A
AENLWVPVY	<u>1050</u>	9	HIV	gp120	1	A
AENLWVDVY	<u>1051</u>	9	HIV	gp120	1	A
AENLWVNVY	<u>1052</u>	9	HIV	gp120	1	A
AENLWVSIVY	<u>1053</u>	9	HIV	gp120	1	A
AENLWVTFY	<u>1054</u>	9	HIV	gp120	1	A
AENLWVTLY	<u>1055</u>	9	HIV	gp120	1	A
AENLWVTPY	<u>1056</u>	9	HIV	gp120	1	A
AENLWVTDY	<u>1057</u>	9	HIV	gp120	1	A
AENLWVTNY	<u>1058</u>	9	HIV	gp120	1	A
AENLWVTIY	<u>1059</u>	9	HIV	gp120	1	A
AENLWVTVA	<u>1060</u>	9	HIV	gp120	1	A
AENLWVTVC	<u>1061</u>	9	HIV	gp120	1	A
AENLWVTVE	<u>1062</u>	9	HIV	gp120	1	A
AENLWVTVF	<u>1063</u>	9	HIV	gp120	1	A
AENLWVTVG	<u>1064</u>	9	HIV	gp120	1	A
AENLWVTVH	<u>1065</u>	9	HIV	gp120	1	A
AENLWVTVI	<u>1066</u>	9	HIV	gp120	1	A
AENLWVTVL	<u>1067</u>	9	HIV	gp120	1	A
AENLWVTVM	<u>1068</u>	9	HIV	gp120	1	A
AENLWVTVN	<u>1069</u>	9	HIV	gp120	1	A
AENLWVTVP	<u>1070</u>	9	HIV	gp120	1	A
AENLWVTVQ	<u>1071</u>	9	HIV	gp120	1	A

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
AENLWVTVR	<u>1072</u>	9	HIV	gp120	1	A
AENLWVTVS	<u>1073</u>	9	HIV	gp120	1	A
AENLWVTVT	<u>1074</u>	9	HIV	gp120	1	A
AENLWVTVV	<u>1075</u>	9	HIV	gp120	1	A
AENLWVTVW	<u>1076</u>	9	HIV	gp120	1	A
AENLWVTVY	<u>1077</u>	9	HIV	gp120	1	
AENLYVTVF	<u>1078</u>	9	HIV	gp120	1	A
TEPAAVGVGAV	<u>1079</u>	11	HIV	NEF	33	
AEPAAEVGV	<u>1080</u>	8	HIV	NEF	34	
AEPAAEVGVGA	<u>1081</u>	10	HIV	NEF	34	
AEPAAEVGVGAV	<u>1082</u>	11	HIV	NEF	34	
QEEEEVGFPV	<u>1083</u>	10	HIV	NEF	84	
EEEEVGFPV	<u>1084</u>	9	HIV	NEF	86	
EEEVGFPV	<u>1085</u>	8	HIV	NEF	87	
EEVGFPVRPQV	<u>1086</u>	11	HIV	NEF	88	
DEEVGFPV	<u>1087</u>	8	HIV	NEF	89	
KEKGGLDGL	<u>1088</u>	9	HIV	NEF	120	
KEKGGLDGLI	<u>1089</u>	10	HIV	NEF	120	
QEILDLWV	<u>1090</u>	8	HIV	NEF	184	
QEILDLWVY	<u>1091</u>	9	HIV	NEF	184	
AETFYVDGA	<u>1092</u>	9	HIV	POL	629	
EKPRTLHDL	<u>1093</u>	10	HPV	E6	6	
NEILIRCII	<u>1094</u>	9	HPV	E6	97	
QEKKRHVDL	<u>1095</u>	9	HPV	E6	113	
AEGKEVLL	<u>1096</u>	8	Human	CEA	46	
QELFIPNI	<u>1097</u>	8	Human	CEA	282	
QELFISNI	<u>1098</u>	8	Human	CEA	460	
TEKNSGLY	<u>1099</u>	8	Human	CEA	468	
AELPKPSI	<u>1100</u>	8	Human	CEA	498	
PEAQNTTY	<u>1101</u>	8	Human	CEA	525	
IESTPFNVA	<u>1102</u>	9	Human	CEA	38	
AEGKEVLLL	<u>1103</u>	9	Human	CEA	46	
EEATGQFRV	<u>1104</u>	9	Human	CEA	132	
VEDKDAVAF	<u>1105</u>	9	Human	CEA	157	
CEPETQDAT	<u>1106</u>	9	Human	CEA	167	
PETQDATYL	<u>1107</u>	9	Human	CEA	169	
CETQNPVSA	<u>1108</u>	9	Human	CEA	215	
QELFIPNIT	<u>1109</u>	9	Human	CEA	282	
AEPPKPFIT	<u>1110</u>	9	Human	CEA	320	
VEDEDAVAL	<u>1111</u>	9	Human	CEA	335	
CEPEIQNTT	<u>1112</u>	9	Human	CEA	345	
PEIQNTTYL	<u>1113</u>	9	Human	CEA	347	
YECGIQNEL	<u>1114</u>	9	Human	CEA	391	
QELFISNIT	<u>1115</u>	9	Human	CEA	460	
TEKNSGLYT	<u>1116</u>	9	Human	CEA	468	
AEGKEVLLL	<u>1117</u>	10	Human	CEA	46	
KEVLLLVHNL	<u>1118</u>	10	Human	CEA	49	
GERVDGNRQI	<u>1119</u>	10	Human	CEA	70	
REIIYPNASL	<u>1120</u>	10	Human	CEA	98	
NEEATGQFRV	<u>1121</u>	10	Human	CEA	131	
EEATGQFRVY	<u>1122</u>	10	Human	CEA	132	

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
GENLNLSCHA	<u>1123</u>	10	Human	CEA	252	
QELFIPNITV	<u>1124</u>	10	Human	CEA	282	
CEPEIQNTTY	<u>1125</u>	10	Human	CEA	345	
PEIQNTTYLW	<u>1126</u>	10	Human	CEA	347	
CEPEAQNTTY	<u>1127</u>	10	Human	CEA	523	
PEAQNTTYLW	<u>1128</u>	10	Human	CEA	525	
MESPSAPPHRW	<u>1129</u>	11	Human	CEA	1	
IESTPFNVAEG	<u>1130</u>	11	Human	CEA	38	
GERVDGNRQII	<u>1131</u>	11	Human	CEA	70	
REIIYPNASLL	<u>1132</u>	11	Human	CEA	98	
NEEATGQFRVY	<u>1133</u>	11	Human	CEA	131	
CEPETQDATYL	<u>1134</u>	11	Human	CEA	167	
GENLNLSCHAA	<u>1135</u>	11	Human	CEA	252	
CEPEIQNTTYL	<u>1136</u>	11	Human	CEA	345	
PEIQNTTYLWW	<u>1137</u>	11	Human	CEA	347	
YECGIQNELSV	<u>1138</u>	11	Human	CEA	391	
NELSVDHSDPV	<u>1139</u>	11	Human	CEA	397	
CEPEAQNTTYL	<u>1140</u>	11	Human	CEA	523	
PEAQNTTYLWW	<u>1141</u>	11	Human	CEA	525	
PEIQNTTYLWWV	<u>1142</u>	12	Human	CEA	347	
PEAQNTTYLWW		12	Human	CEA	525	
V	<u>1143</u>					
CEPEIQNTTYLW		13	Human	CEA	345	
W	<u>1144</u>					
AEMGKGSFKY	<u>1145</u>	10	Human	elong. Factor Tu	48	
SEDCQSL	<u>1146</u>	7	Human	Her2/neu	209	
REVRAVT	<u>1147</u>	7	Human	Her2/neu	351	
FETLEEI	<u>1148</u>	7	Human	Her2/neu	400	
TELVEPL	<u>1149</u>	7	Human	Her2/neu	694	
SECRPRF	<u>1150</u>	7	Human	Her2/neu	963	
PETHLDM	<u>1151</u>	8	Human	Her2/neu	39	
QEVQGYVL	<u>1152</u>	8	Human	Her2/neu	78	
RELQLRSL	<u>1153</u>	8	Human	Her2/neu	138	
CELHCPAL	<u>1154</u>	8	Human	Her2/neu	264	
LEEITGYL	<u>1155</u>	8	Human	Her2/neu	403	
EEITGYLY	<u>1156</u>	8	Human	Her2/neu	404	
DECVGEGL	<u>1157</u>	8	Human	Her2/neu	502	
AEQRASPL	<u>1158</u>	8	Human	Her2/neu	644	
KEILDEAY	<u>1159</u>	8	Human	Her2/neu	765	
EEAPRSPL	<u>1160</u>	8	Human	Her2/neu	1068	
SEDPTVPL	<u>1161</u>	8	Human	Her2/neu	1113	
MELAALCRW	<u>1162</u>	9	Human	Her2/neu	1	
QEVQGYVLI	<u>1163</u>	9	Human	Her2/neu	78	
FEDNYALAV	<u>1164</u>	9	Human	Her2/neu	108	
RELQLRSLT	<u>1165</u>	9	Human	Her2/neu	138	
TEILKGGVL	<u>1166</u>	9	Human	Her2/neu	146	
HEQCAAGCT	<u>1167</u>	9	Human	Her2/neu	237	
CELHCPALV	<u>1168</u>	9	Human	Her2/neu	264	
FESMPNPEG	<u>1169</u>	9	Human	Her2/neu	279	
QEVTAEDGT	<u>1170</u>	9	Human	Her2/neu	320	
CEKCSKPCA	<u>1171</u>	9	Human	Her2/neu	331	
MEHLREVRA	<u>1172</u>	9	Human	Her2/neu	347	

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
REVRVAVTSA	<u>1173</u>	9	Human	Her2/neu	351	
QEFAGCKKI	<u>1174</u>	9	Human	Her2/neu	362	
EEITGYLYI	<u>1175</u>	9	Human	Her2/neu	404	
RELGSGLAL	<u>1176</u>	9	Human	Her2/neu	459	
GEGlachQL	<u>1177</u>	9	Human	Her2/neu	506	
QECVEECRV	<u>1178</u>	9	Human	Her2/neu	538	
VEECRVLQG	<u>1179</u>	9	Human	Her2/neu	541	
EECRVLQGL	<u>1180</u>	9	Human	Her2/neu	542	
AEQRASPLT	<u>1181</u>	9	Human	Her2/neu	644	
QETELVEPL	<u>1182</u>	9	Human	Her2/neu	692	
VEPLTPSGA	<u>1183</u>	9	Human	Her2/neu	697	
TELKVKVL	<u>1184</u>	9	Human	Her2/neu	718	
GENVKIPVA	<u>1185</u>	9	Human	Her2/neu	743	
KEILDEAYV	<u>1186</u>	9	Human	Her2/neu	765	
DEAYVMAGV	<u>1187</u>	9	Human	Her2/neu	769	
DETEYHADG	<u>1188</u>	9	Human	Her2/neu	873	
LESILRRRF	<u>1189</u>	9	Human	Her2/neu	891	
GERLPQPI	<u>1190</u>	9	Human	Her2/neu	938	
LEDDDMGDL	<u>1191</u>	9	Human	Her2/neu	1009	
EEYLVQQG	<u>1192</u>	9	Human	Her2/neu	1021	
EEEAPRSPL	<u>1193</u>	9	Human	Her2/neu	1067	
EEAPRSPLA	<u>1194</u>	9	Human	Her2/neu	1068	
SEGAGSDVF	<u>1195</u>	9	Human	Her2/neu	1078	
PEYVNQPDV	<u>1196</u>	9	Human	Her2/neu	1137	
PEYLTPQGG	<u>1197</u>	9	Human	Her2/neu	1194	
PERGAPPST	<u>1198</u>	9	Human	Her2/neu	1228	
AENPEYLGL	<u>1199</u>	9	Human	Her2/neu	1243	
MELAALCRWG	<u>1200</u>	10	Human	Her2/neu	1	
LELYLPTNA	<u>1201</u>	10	Human	Her2/neu	60	
QEVQGYVLI	<u>1202</u>	10	Human	Her2/neu	78	
FEDNYALAVL	<u>1203</u>	10	Human	Her2/neu	108	
TEILKGGVLI	<u>1204</u>	10	Human	Her2/neu	146	
GESSEDCQSL	<u>1205</u>	10	Human	Her2/neu	206	
SEDCQSLTRT	<u>1206</u>	10	Human	Her2/neu	209	
CELHCPALVT	<u>1207</u>	10	Human	Her2/neu	264	
MEHLREVRAV	<u>1208</u>	10	Human	Her2/neu	347	
QEFAGCKKIF	<u>1209</u>	10	Human	Her2/neu	362	
FETLEEITGY	<u>1210</u>	10	Human	Her2/neu	400	
LEEITGYLYI	<u>1211</u>	10	Human	Her2/neu	403	
RELGSGLALI	<u>1212</u>	10	Human	Her2/neu	459	
PEDECVGEG	<u>1213</u>	10	Human	Her2/neu	500	
QECVEECRVL	<u>1214</u>	10	Human	Her2/neu	538	
VEECRVLQGL	<u>1215</u>	10	Human	Her2/neu	541	
REYVNARHCL	<u>1216</u>	10	Human	Her2/neu	552	
PECQPQNGSV	<u>1217</u>	10	Human	Her2/neu	565	
BEGACQPCPI	<u>1218</u>	10	Human	Her2/neu	619	
QETELVEPLT	<u>1219</u>	10	Human	Her2/neu	692	
VEPLTPSGAM	<u>1220</u>	10	Human	Her2/neu	697	
KETELRKVKV	<u>1221</u>	10	Human	Her2/neu	716	
TELKVKVLG	<u>1222</u>	10	Human	Her2/neu	718	
GENVKIPVAI	<u>1223</u>	10	Human	Her2/neu	743	

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
KEILDEAYVM	<u>1224</u>	10	Human	Her2/neu	765	
DEAYVMAGVG	<u>1225</u>	10	Human	Her2/neu	769	
DETEYHADGG	<u>1226</u>	10	Human	Her2/neu	873	
TEYHADGGKV	<u>1227</u>	10	Human	Her2/neu	875	
LESILRRRFT	<u>1228</u>	10	Human	Her2/neu	891	
REIPDLLEKG	<u>1229</u>	10	Human	Her2/neu	929	
SECRPRFREL	<u>1230</u>	10	Human	Her2/neu	963	
RELVSEFSRM	<u>1231</u>	10	Human	Her2/neu	970	
NEDLGASPL	<u>1232</u>	10	Human	Her2/neu	991	
AEEYLVQQG	<u>1233</u>	10	Human	Her2/neu	1020	
EEYLVQQGF	<u>1234</u>	10	Human	Her2/neu	1021	
SEEEAPRSPL	<u>1235</u>	10	Human	Her2/neu	1066	
EEEAPRSPLA	<u>1236</u>	10	Human	Her2/neu	1067	
SETDGYVAPL	<u>1237</u>	10	Human	Her2/neu	1122	
PERGAPPSTF	<u>1238</u>	10	Human	Her2/neu	1228	
PEYLGLDVPV	<u>1239</u>	10	Human	Her2/neu	1246	
MELAALCRWGL	<u>1240</u>	11	Human	Her2/neu	1	
PETHLDMLRHL	<u>1241</u>	11	Human	Her2/neu	39	
RELQLRSLTEI	<u>1242</u>	11	Human	Her2/neu	138	
GESSEDCQSLT	<u>1243</u>	11	Human	Her2/neu	206	
SEDCQSLTRTV	<u>1244</u>	11	Human	Her2/neu	209	
CELHCPALVTY	<u>1245</u>	11	Human	Her2/neu	264	
FESMPNPEGRY	<u>1246</u>	11	Human	Her2/neu	279	
CEKCSKPCARV	<u>1247</u>	11	Human	Her2/neu	331	
MEHLREVRAVT	<u>1248</u>	11	Human	Her2/neu	347	
REVRAVTSANI	<u>1249</u>	11	Human	Her2/neu	351	
QEFAGCKKIFG	<u>1250</u>	11	Human	Her2/neu	362	
FETLEEITGYL	<u>1251</u>	11	Human	Her2/neu	400	
EEITGYLYISA	<u>1252</u>	11	Human	Her2/neu	404	
GEGLACHQLCA	<u>1253</u>	11	Human	Her2/neu	506	
DEEGACQPCPI	<u>1254</u>	11	Human	Her2/neu	618	
AEQRASPLTSI	<u>1255</u>	11	Human	Her2/neu	644	
TELVEPLTPSG	<u>1256</u>	11	Human	Her2/neu	694	
KETELRKVKVL	<u>1257</u>	11	Human	Her2/neu	716	
KEILDEAYVMA	<u>1258</u>	11	Human	Her2/neu	765	
LEDVRLVHRDL	<u>1259</u>	11	Human	Her2/neu	836	
WELMTFGAKPY	<u>1260</u>	11	Human	Her2/neu	913	
GERLPQPICT	<u>1261</u>	11	Human	Her2/neu	938	
SECRPRFREL	<u>1262</u>	11	Human	Her2/neu	963	
RELVSEFSRMA	<u>1263</u>	11	Human	Her2/neu	970	
AEEYLVQQGF	<u>1264</u>	11	Human	Her2/neu	1020	
EEYLVQQGFF	<u>1265</u>	11	Human	Her2/neu	1021	
SEEEAPRSPLA	<u>1266</u>	11	Human	Her2/neu	1066	
SEGAGSDVFDG	<u>1267</u>	11	Human	Her2/neu	1078	
SETDGYVAPLT	<u>1268</u>	11	Human	Her2/neu	1122	
REGPLPAARPA	<u>1269</u>	11	Human	Her2/neu	1153	
VENPEYLTPQG	<u>1270</u>	11	Human	Her2/neu	1191	
PEYLTPQGGAA	<u>1271</u>	11	Human	Her2/neu	1194	
AENPEYLGLDV	<u>1272</u>	11	Human	Her2/neu	1243	
LELTYLPTNASL	<u>1273</u>	12	Human	Her2/neu	60	
RELQLRSLTEIL	<u>1274</u>	12	Human	Her2/neu	138	

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
PEGRYTFGASCV	<u>1275</u>	12	Human	Her2/neu	285	
LEEITGYLYISA	<u>1276</u>	12	Human	Her2/neu	403	
EEITGYLYISAW	<u>1277</u>	12	Human	Her2/neu	404	
PEADQCVACAH Y	<u>1278</u>	12	Human	Her2/neu	579	
TELVEPLTPSGA	<u>1279</u>	12	Human	Her2/neu	694	
TEYHADGGKVPI	<u>1280</u>	12	Human	Her2/neu	875	
GERLPQPPICTI	<u>1281</u>	12	Human	Her2/neu	938	
AEEYLVPQQGFF	<u>1282</u>	12	Human	Her2/neu	1020	
PEGRYTFGASCV T	<u>1283</u>	13	Human	Her2/neu	285	
CEKCSKPCARVC Y	<u>1284</u>	13	Human	Her2/neu	331	
MEHLREVRAVTS A	<u>1285</u>	13	Human	Her2/neu	347	
DECVGEGLACHQ L	<u>1286</u>	13	Human	Her2/neu	502	
PECQPQNGSVTC F	<u>1287</u>	13	Human	Her2/neu	565	
RENTSPKANKEIL	<u>1288</u>	13	Human	Her2/neu	756	
REIPDLLEKGERL	<u>1289</u>	13	Human	Her2/neu	929	
SEFSRMARDPQR F	<u>1290</u>	13	Human	Her2/neu	974	
SEGAGSDVFDGD L	<u>1291</u>	13	Human	Her2/neu	1078	
GEFGGYGSV	<u>1292</u>	9	Human	Histactranf	127	A
LWQLNGRLEYTL KDR	<u>1293</u>	15	Human	IFN-B	21	A
SEFQAAI	<u>1294</u>	7	Human	MAGE2	103	
SEYLQLV	<u>1295</u>	7	Human	MAGE2	155	
WEELSML	<u>1296</u>	7	Human	MAGE2	222	
GEPHISY	<u>1297</u>	7	Human	MAGE2	295	
LEARGEAL	<u>1298</u>	8	Human	MAGE2	16	
QEEEGPRM	<u>1299</u>	8	Human	MAGE2	90	
EEEGPRMF	<u>1300</u>	8	Human	MAGE2	91	
VELVHFL	<u>1301</u>	8	Human	MAGE2	114	
AEMLESVL	<u>1302</u>	8	Human	MAGE2	133	
SEYLQLVF	<u>1303</u>	8	Human	MAGE2	155	
EKIWEEL	<u>1304</u>	8	Human	MAGE2	218	
LEARGEALG	<u>1305</u>	9	Human	MAGE2	16	
GEALGLVGA	<u>1306</u>	9	Human	MAGE2	20	
QEEEGPRMF	<u>1307</u>	9	Human	MAGE2	90	
VELVHFLLL	<u>1308</u>	9	Human	MAGE2	114	
REPVTKAEM	<u>1309</u>	9	Human	MAGE2	127	
SEYLQLVFG	<u>1310</u>	9	Human	MAGE2	155	
PEEKIWEEL	<u>1311</u>	9	Human	MAGE2	217	
EELSMLEVF	<u>1312</u>	9	Human	MAGE2	223	
FEGREDSVF	<u>1313</u>	9	Human	MAGE2	231	
YEFLWGPR	<u>1314</u>	9	Human	MAGE2	269	
EEGLEARGEAL	<u>1315</u>	10	Human	MAGE2	13	
LEARGEALGL	<u>1316</u>	10	Human	MAGE2	16	
VEVTLGEVPA	<u>1317</u>	10	Human	MAGE2	46	
EEGPRMFDDL	<u>1318</u>	10	Human	MAGE2	92	

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
REPVTKAEML	<u>1319</u>	10	Human	MAGE2	127	
SEYLQLVFGI	<u>1320</u>	10	Human	MAGE2	155	
VEVVPISHLY	<u>1321</u>	10	Human	MAGE2	167	
EEKIWEELSM	<u>1322</u>	10	Human	MAGE2	218	
WEELSMLEVF	<u>1323</u>	10	Human	MAGE2	222	
FEGREDSVFA	<u>1324</u>	10	Human	MAGE2	231	
QENYLEYRQV	<u>1325</u>	10	Human	MAGE2	252	
YEFLWGPRAL	<u>1326</u>	10	Human	MAGE2	269	
GEPHISYPPL	<u>1327</u>	10	Human	MAGE2	295	
EEGLEARGEAL	<u>1328</u>	11	Human	MAGE2	13	
LEARGEALGLV	<u>1329</u>	11	Human	MAGE2	16	
GEALGLVGAQA	<u>1330</u>	11	Human	MAGE2	20	
EEQQTASSSST	<u>1331</u>	11	Human	MAGE2	34	
VEVTLGEVPAA	<u>1332</u>	11	Human	MAGE2	46	
EEEGPRMFPDL	<u>1333</u>	11	Human	MAGE2	91	
SEFQAAISRKM	<u>1334</u>	11	Human	MAGE2	103	
VELVHFLLLKY	<u>1335</u>	11	Human	MAGE2	114	
LESVLRNCQDF	<u>1336</u>	11	Human	MAGE2	136	
VEVVPISHLYI	<u>1337</u>	11	Human	MAGE2	167	
IEGDCAPEEKI	<u>1338</u>	11	Human	MAGE2	211	
EEKIWEELSM	<u>1339</u>	11	Human	MAGE2	218	
EELSMLEVFEG	<u>1340</u>	11	Human	MAGE2	223	
LEVFEGRDSV	<u>1341</u>	11	Human	MAGE2	228	
YEFLWGPRALI	<u>1342</u>	11	Human	MAGE2	269	
EEQQTASSSSTL	<u>1343</u>	12	Human	MAGE2	34	
QEEEGPRMFPDL	<u>1344</u>	12	Human	MAGE2	90	
SEFQAAISRKMV	<u>1345</u>	12	Human	MAGE2	103	
LESVLRNCQDFF	<u>1346</u>	12	Human	MAGE2	136	
VEVVPISHLYIL	<u>1347</u>	12	Human	MAGE2	167	
EEGLEARGEALG	<u>1348</u>	13	Human	MAGE2	13	
L						
LEARGEALGLVG	<u>1349</u>	13	Human	MAGE2	16	
A						
LESEFQAAISRK	<u>1350</u>	13	Human	MAGE2	101	
M						
REPVTKAEMLES	<u>1351</u>	13	Human	MAGE2	127	
V						
SEYLQLVFGIEVV	<u>1352</u>	13	Human	MAGE2	155	
IEVVEVVPISHLY	<u>1353</u>	13	Human	MAGE2	164	
VEVVPISHLYILV	<u>1354</u>	13	Human	MAGE2	167	
MEVDPIGHLV	<u>1355</u>	10	Human	MAGE3	167	
EEEGPSTF	<u>1356</u>	8	Human	MAGE3	91	
AELVHFL	<u>1357</u>	8	Human	MAGE3	114	
FEGREDSEI	<u>1358</u>	8	Human	MAGE3	231	
QEAASSSST	<u>1359</u>	9	Human	MAGE3	36	
AELVHFLLL	<u>1360</u>	9	Human	MAGE3	114	
AEMLGSVVG	<u>1361</u>	9	Human	MAGE3	133	
EELSVLEVF	<u>1362</u>	9	Human	MAGE3	223	
FEGREDSIL	<u>1363</u>	9	Human	MAGE3	231	
QEAASSSSTL	<u>1364</u>	10	Human	MAGE3	36	
EEGPSTFPDL	<u>1365</u>	10	Human	MAGE3	92	
IELMEVDPIG	<u>1366</u>	10	Human	MAGE3	164	

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
MEVDPIGHLY	<u>1367</u>	10	Human	MAGE3	167	
EKIWEELSV	<u>1368</u>	10	Human	MAGE3	218	
WEELSVLEVF	<u>1369</u>	10	Human	MAGE3	222	
FEGREDSILG	<u>1370</u>	10	Human	MAGE3	231	
EEEGPSTFPDL	<u>1371</u>	11	Human	MAGE3	91	
AELVHFLLLKY	<u>1372</u>	11	Human	MAGE3	114	
MEVDPIGHLYI	<u>1373</u>	11	Human	MAGE3	167	
REGDCAPEEKI	<u>1374</u>	11	Human	MAGE3	211	
EKIWEELSVL	<u>1375</u>	11	Human	MAGE3	218	
LEVFEGREDSI	<u>1376</u>	11	Human	MAGE3	228	
RERFEMF	<u>1377</u>	7	Human	p53	335	
LEDSSGNL	<u>1378</u>	8	Human	p53	257	
GEYFTLQI	<u>1379</u>	8	Human	p53	325	
VEPPLSQET	<u>1380</u>	9	Human	p53	10	
PENNVLSPL	<u>1381</u>	9	Human	p53	27	
DEAPRMPEA	<u>1382</u>	9	Human	p53	61	
HERCSDSDG	<u>1383</u>	9	Human	p53	179	
VEGNLRVEY	<u>1384</u>	9	Human	p53	197	
VEYLDDRNT	<u>1385</u>	9	Human	p53	203	
LEDSSGNLL	<u>1386</u>	9	Human	p53	257	
RELNEALEL	<u>1387</u>	9	Human	p53	342	
NEALELKDA	<u>1388</u>	9	Human	p53	345	
LELKDAQAG	<u>1389</u>	9	Human	p53	348	
MEEPQSDPSV	<u>1390</u>	10	Human	p53	1	
VEPPLSQETF	<u>1391</u>	10	Human	p53	10	
QETFSDLWKL	<u>1392</u>	10	Human	p53	16	
IEQWFTEDPG	<u>1393</u>	10	Human	p53	50	
DEAPRMPEAA	<u>1394</u>	10	Human	p53	61	
HERCSDSDGL	<u>1395</u>	10	Human	p53	179	
VEGNLRVEYL	<u>1396</u>	10	Human	p53	197	
VEYLDDRNTF	<u>1397</u>	10	Human	p53	203	
PEVGSDCTTI	<u>1398</u>	10	Human	p53	223	
LEDSSGNLLG	<u>1399</u>	10	Human	p53	257	
FEVRVCACPG	<u>1400</u>	10	Human	p53	270	
TEENLRKKG	<u>1401</u>	10	Human	p53	284	
GEPHHELPPG	<u>1402</u>	10	Human	p53	293	
GEYFTLQIRG	<u>1403</u>	10	Human	p53	325	
RERFEMFREL	<u>1404</u>	10	Human	p53	335	
FEMFRELNEA	<u>1405</u>	10	Human	p53	338	
QETFSDLWKLL	<u>1406</u>	11	Human	p53	16	
HERCSDSDGLA	<u>1407</u>	11	Human	p53	179	
YEPPEVGSDCT	<u>1408</u>	11	Human	p53	220	
HELPPGSTKRA	<u>1409</u>	11	Human	p53	297	
FEMFRELNEAL	<u>1410</u>	11	Human	p53	338	
NEALELKDAQA	<u>1411</u>	11	Human	p53	345	
TEDPGPDEAPRM	<u>1412</u>	12	Human	p53	55	
GEPHHELPPGST	<u>1413</u>	12	Human	p53	293	
DEAPRMPEAAPP	<u>1414</u>	13	Human	p53	61	
V	<u>1414</u>					
YEPPEVGSDCTTI	<u>1415</u>	13	Human	p53	220	
RERRDNYV	<u>1416</u>	8	Human	unknown		

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
SEIDLILGY	<u>1417</u>	9	Human	unknown		
AEIPTRVNY	<u>1418</u>	9	Human	unknown		
AEMGKFKFSY	<u>1419</u>	10	Human	unknown		
DEIGVIDLY	<u>1420</u>	9	Human	unknown		
AEMGKFKYSF	<u>1421</u>	10	Human	unknown		A
SEAIHTFQY	<u>1422</u>	9	Human	unknown		
SEAIYTFQF	<u>1423</u>	9	Human	unknown		A
AEGIVTGQY	<u>1424</u>	9	Human	unknown		
HETTYNSI	<u>1425</u>	8	Mouse	beta actin	275	A
GELSYLNV	<u>1426</u>	8	Mouse	cathepsin D	255	
YEDTGKTI	<u>1427</u>	8	Mouse	p40 phox RNA	245	
YENDIEKKI	<u>1428</u>	9	Pf	CSP	375	

TABLE 22

HLA-B44 SUPERTYPE							
Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
SEAAAYAKKI	<u>983</u>	8609	308	129	1685	61	287
GEFPYKAAA	<u>984</u>	286	170	3.9	746	2537	11
SEAPYKAIL	<u>985</u>	2258	29	8.8	440	170	262
SEAPKYAIL	<u>986</u>	2263	113	7.8	762	2260	479
AEFKYIAAV	<u>987</u>	48	2.8	6.5	28	21	4.9
AEIPYLAKY	<u>988</u>	116	7258	3159	44	30	668
AEIPKLAYF	<u>989</u>	1641	57	5.6	229	57	608
FPPDYAAAF	<u>990</u>	141					
FPPKYKAAF	<u>991</u>	155					
FPPKYAKAF	<u>992</u>	86					
FPPKYAAAF	<u>993</u>	16					
FAFKYAAAF	<u>994</u>	95					
FQFKYAAAF	<u>995</u>	22					
FDFKYAAAF	<u>996</u>	187					
SENDRYRL	<u>997</u>	18281	271	23	183	164	1073
IEDPPYNSL	<u>998</u>	35457	16	688	15833	40075	18697
YEANGNLI	<u>999</u>	191	7.9	7.0	516	3085	10342
YEDLRVLSF	<u>1000</u>	20	67	71	24	212	18697
SDYEGRLI	<u>1001</u>	>24800	27150	86	851	228	10469
GEISPYPSL	<u>1002</u>	19361	24	1.8	3564	293	115
MDIDPYKEF	<u>1003</u>	169477	3700	382	21744	1949	2615
LDKGIPY	<u>1004</u>	>100000	17884	468	>43192.49	19311	23609
ADLMGYIPL	<u>1005</u>	>7616.71	959	4.7	>21395.35	10292	>49000
LDPYARVAI	<u>1006</u>	>24409.45	>88888.89	372	>41628.96	>39766.08	>49000
AENLWVTVY	<u>1007</u>	155	1053	547	522	284	200
KENLWVTVY	<u>1008</u>	184	2738	373	308	306	6215
AEKLWVTVY	<u>1009</u>	286	18278	306	168	287	219
AENKWVTVY	<u>1010</u>	781	11303	534	294	540	297
AENLKVTVY	<u>1011</u>	138	7746	1075	253	487	9624
AENLWKTVY	<u>1012</u>	913	850	406	139	383	245
AENLWVKVY	<u>1013</u>	2735	1482	1696	708	105	132
AENLWVTKY	<u>1014</u>	511	1010	1998	355	1064	201
AENLWVTVK	<u>1015</u>	29464	853	2004	6305	2133	186
FENLWVTVY	<u>1016</u>	59	943	1336	4179	1312	21403
VENLWVTVY	<u>1017</u>	25	5499	5586	13454	4856	15654
PENLWVTVY	<u>1018</u>	190	>72727.27	>154545.45	>167272.73	>425000	>49000
NENLWVTVY	<u>1019</u>	38	>72727.27	11774	453	224	1668
DENLWVTVY	<u>1020</u>	26	>72727.27	41098	4589	988	49000
TENLWVTVY	<u>1021</u>	14	14040	1415	291	364	5296
YENLWVTVY	<u>1022</u>	29	552	324	640	369	10701
ATNLWVTVY	<u>1023</u>	17615	487	>154545.45	8912	>43037.97	>49000
AEFLWVTVY	<u>1024</u>	131	183	240	1013	156	472
AEVLWVTVY	<u>1025</u>	142	1549	436	1520	390	1244
AEPLWVTVY	<u>1026</u>	310	1727	2484	1322	96	1384
AEDLWVTVY	<u>1027</u>	354	423	3521	2329	469	1845
AENLWVTVY	<u>1028</u>	122	1581	552	308	132	301
AETLWVTVY	<u>1029</u>	199	1052	198	501	221	774
AENFWVTVY	<u>1030</u>	182	1394	542	171	268	289
AENVWVTVY	<u>1031</u>	262	2238	386	1112	744	737
AENPWVTVY	<u>1032</u>	27	843	224	18	53	202

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Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
AENDWVTVY	<u>1033</u>	324	954	742	96	165	365
AENNWVTVY	<u>1034</u>	167	1161	357	214	162	99
AENTWVTVY	<u>1035</u>	213	1451	1793	386	166	442
AENLFVTVY	<u>1036</u>	29	970	334	357	125	232
AENLVVTVY	<u>1037</u>	62	876	1344	1030	203	718
AENLPVTVY	<u>1038</u>	20	205	566	356	126	246
AENLDVTVY	<u>1039</u>	517	220	12081	673	340	1291
AENLNVTY	<u>1040</u>	198	564	3544	447	358	2445
AENLTVTVY	<u>1041</u>	153	689	1269	327	208	793
AENLWFTVY	<u>1042</u>	360	699	668	227	62	90
AENLWLTVY	<u>1043</u>	666	1702	884	647	226	227
AENLWPTVY	<u>1044</u>	661	690	688	157	50	116
AENLWDTVY	<u>1045</u>	775	1145	2090	414	68	263
AENLWNTVY	<u>1046</u>	336	1338	957	66	81	257
AENLWTTVY	<u>1047</u>	196	246	625	51	50	118
AENLWVFVY	<u>1048</u>	242	857	375	348	310	237
AENLWVVVY	<u>1049</u>	326	2728	1688	599	632	468
AENLWVPVY	<u>1050</u>	303	175	183	96	47	106
AENLWVDVY	<u>1051</u>	415	700	3440	334	92	242
AENLWVNVY	<u>1052</u>	317	1156	952	159	76	266
AENLWVSVY	<u>1053</u>	232	1251	1347	351	178	292
AENLWVTFY	<u>1054</u>	1299	1201	295	124	222	347
AENLWVTLY	<u>1055</u>	392	463	731	199	119	349
AENLWVTPY	<u>1056</u>	41	274	189	127	44	122
AENLWVTDY	<u>1057</u>	1001	930	1208	191	103	328
AENLWVTNY	<u>1058</u>	730	865	948	149	74	215
AENLWVTTY	<u>1059</u>	28	280	191	37	26	48
AENLWVTVA	<u>1060</u>	9689	557	4.8	1543	296	9.1
AENLWVTVC	<u>1061</u>	178026	157	1425	5593	2267	146
AENLWVTVE	<u>1062</u>	>258333.33	3888	1362	8910	2573	246
AENLWVTVF	<u>1063</u>	365	162	20	346	162	262
AENLWVTVG	<u>1064</u>	39743	861	47	1812	245	35
AENLWVTVH	<u>1065</u>	16516	493	151	966	387	120
AENLWVTVI	<u>1066</u>	11224	14	7.3	237	88	54
AENLWVTVL	<u>1067</u>	6198	14	13	68	208	114
AENLWVTVM	<u>1068</u>	508	13	6.1	195	35	50
AENLWVTVN	<u>1069</u>	129167	6701	481	2623	414	169
AENLWVTVP	<u>1070</u>	38441	9711	339	7715	2473	187
AENLWVTVQ	<u>1071</u>	49640	522	85	1223	188	100
AENLWVTVR	<u>1072</u>	32979	1246	1744	4857	1474	233
AENLWVTVS	<u>1073</u>	25726	2163	103	4221	417	34
AENLWVTVT	<u>1074</u>	12331	947	7.8	2696	343	10
AENLWVTVV	<u>1075</u>	10709	84	19	5757	1432	35
AENLWVTVW	<u>1076</u>	22610	1304	135	423	324	204
AENLWVTVY	<u>1077</u>	51	1358	90	66	43	68
AENLYVTVF	<u>1078</u>	61	17	3.1	39	47	69
TEPAAVGVGAV	<u>1079</u>	>8115.18	930	391	1938	459	8235
AEPAAEV	<u>1080</u>	>8115.18	2070	2675	>22604.42	402	6590
AEPAAEVGVA	<u>1081</u>	>8115.18	4116	1655	>22604.42	>11447.81	104
AEPAAEVGAV	<u>1082</u>	>8611.11	20364	242	>23896.1	>11447.81	1499
QEEEEVGFPV	<u>1083</u>	>8611.11	13117	2596	15203	>11447.81	86
EEEEVGFPV	<u>1084</u>	3691	3340	417	7440	10313	37

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Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
EEVVGFPV	<u>1085</u>	427	9578	2605	6372	>10461.54	227
EEVGFPVRPQV	<u>1086</u>	>22794.12	9905	108	23777	6553	808
DEEVGFPV	<u>1087</u>	7.1	>32000	4260	9305	>10461.54	916
KEKGGLDGL	<u>1088</u>	>22794.12	55	174	>81415.93	>10461.54	9926
KEKGGLDGLI	<u>1089</u>	>22794.12	843	233	14726	3626	9986
QEILDLWV	<u>1090</u>	>22794.12	142	1717	>81415.93	5919	5504
QEILDLWVY	<u>1091</u>	52	740	4522	264	172	6261
AETFYVDGA	<u>1092</u>	>6709.96	21630	1923	>21198.16	6924	38
EEKPRTLHDL	<u>1093</u>	>81578.95	36208	34027	15236	30010	419
NEILIRCI	<u>1094</u>	5672	291	59	2722	258	3248
QEKKRHVLDL	<u>1095</u>	7.3	15984	63093	443	211	12613
AEGKEVLL	<u>1096</u>	11455	1311	5303	17268	129	14165
QELFIPNI	<u>1097</u>	127	5815	147	752	8.5	1319
QELFISNI	<u>1098</u>	889	6396	1175	2282	70	1172
TEKNSGLY	<u>1099</u>	211	9851	7117	1868	605	10248
AELPKPSI	<u>1100</u>	7423	6697	131	1164	19	2608
PEAQNTTY	<u>1101</u>	149	2594	2437	2204	76	3255
IESTPFNVA	<u>1102</u>	69	1234	66	18749	0.97	15
AEGKEVLLL	<u>1103</u>	1080	72	147	178	1.7	199
EEATGQFRV	<u>1104</u>	805	5563	470	1691	95	18
VEDKDAVAF	<u>1105</u>	94	121	1583	1661	1443	21204
CEPETQDAT	<u>1106</u>	4009	3646	410	23421	50	97
PETQDATYL	<u>1107</u>	9473	1240	33745	>34586.47	301	13430
CETQNPVSA	<u>1108</u>	73	7016	261	20023	10.0	15
QELFIPNIT	<u>1109</u>	125	4361	172	1217	3.0	18
AEPKPFIT	<u>1110</u>	12850	7067	7170	>34586.47	232	1813
VEDEDAVAL	<u>1111</u>	840	11	2665	30667	51	27810
CEPEIQNTT	<u>1112</u>	6889	5709	3081	31834	120	2732
PEIQNTTYL	<u>1113</u>	923	138	2786	16816	231	1825
YECGIQNEL	<u>1114</u>	82	71	53	452	5.3	855
QELFISNIT	<u>1115</u>	530	6571	58	2334	3.9	80
TEKNSGLYT	<u>1116</u>	1113	7522	3195	10097	101	1963
AEGKEVLLLV	<u>1117</u>	5135	1019	408	479	8.6	994
KEVLLLVHNL	<u>1118</u>	893	3.1	4.4	414	2.3	2512
GERVDGNRQI	<u>1119</u>	9395	1933	369	3900	13	19464
REIYPNASL	<u>1120</u>	741	2.3	7.5	374	1.7	954
NEEATGQFRV	<u>1121</u>	998	29086	22678	4365	471	405
EEATGQFRVY	<u>1122</u>	64	>33333.33	55956	29	1041	1374
GENLNLSCHA	<u>1123</u>	14373	1341	357	8610	5.3	271
QELFIPNITV	<u>1124</u>	81	121	27	93	2.6	14
CEPEIQNTTY	<u>1125</u>	1459	>10322.58	35697	49	14596	43739
PEIQNTTYLW	<u>1126</u>	819	3301	9423	13	6173	10011
CEPEAQNTTY	<u>1127</u>	9525	>12903.23	>48571.43	61	>4268.68	17330
PEAQNTTYLW	<u>1128</u>	17082	>9248.55	>12592.59	27	21243	>28654.97
MESPSAPPHRW	<u>1129</u>	12	943	1915	5.3	41	359
IESTPFNVAEG	<u>1130</u>	87	1074	352	89	8.7	84
GERVDGNRQII	<u>1131</u>	764	278	18	871	1.3	27084
REIYPNASLL	<u>1132</u>	1788	2.4	12	57	0.38	1777
NEEATGQFRVY	<u>1133</u>	7.7	3252	999	9.6	69	3986
CEPETQDATYL	<u>1134</u>	831	311	3388	398	807	62150
GENLNLSCHAA	<u>1135</u>	7838	4557	63	1907	9.0	32
CEPEIQNTTYL	<u>1136</u>	129	287	1603	1245	60	11981

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Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
PEIQNTTYLWW	<u>1137</u>	172	749	1045	17	227	1365
YECGIQNELSV	<u>1138</u>	9.2	33	26	1714	0.46	155
NELSDHSDPV	<u>1139</u>	49	2554	1128	1615	38	78
CEPEAQNTTYL	<u>1140</u>	962	2184	11723	3419	131	2450
PEAQNTTYLWW	<u>1141</u>	147	2096	3090	121	79	2005
PEIQNTTYLWWV	<u>1142</u>	644	1808	1539	481	93	994
PEAQNTTYLWWV	<u>1143</u>	20	1694	646	5.1		3.3
CEPEIQNTTYLW	<u>1144</u>	84	858	3168	7.9	409	1243
W	<u>1144</u>						
AEMGKGSFKY	<u>1145</u>	1618	6427	3820	112	90	305
SEDCQSL	<u>1146</u>	18245	2691	14258	8248	431	19225
REVRVAVT	<u>1147</u>	8564	3136	725	31615	29	23544
FETLEEI	<u>1148</u>	1518	7621	2110	42991	69	67957
TELVEPL	<u>1149</u>	162	14164	1258	8854	66	>148484.85
SECRPRF	<u>1150</u>	926	18181	1157	852	48	8856
PETHLDMML	<u>1151</u>	1954	8387	6118	>17523.81	83	20257
QEVQGYVL	<u>1152</u>	3.4	28	5.0	1210	0.92	33
RELQLRSL	<u>1153</u>	42	49	5.9	2025	0.62	1372
CELHCPAL	<u>1154</u>	150	871	259	4361	39	30089
LEEITGYL	<u>1155</u>	242	830	1805	5913	403	35502
EEITGYLY	<u>1156</u>	20	5713	1223	11	83	238
DECVGEGL	<u>1157</u>	49	4864	481	938	34	14244
AEQRASPL	<u>1158</u>	16	73	13	211	0.38	120
KEILDEAY	<u>1159</u>	82	921	430	1081	74	2646
EEAPRSPL	<u>1160</u>	1191	3489	1611	1593	171	1926
SEDPTVPL	<u>1161</u>	103	71	161	12267	2.0	308
MELAALCRW	<u>1162</u>	7.0	4833	138	16	9.9	1183
QEVQGYVLI	<u>1163</u>	77	206	39	30	0.50	96
FEDNYALAV	<u>1164</u>	12	34	5.1	13470	0.17	131
RELQLRSLT	<u>1165</u>	638	316	13	465	0.20	162
TEILKGGVL	<u>1166</u>	125	30	14	1377	0.28	2480
HEQCAAGCT	<u>1167</u>	1995	42164	7377	19048	178	2974
CELHCPALV	<u>1168</u>	136	4805	319	2308	52	1110
FESMPNPEG	<u>1169</u>	6068	30237	59	16458	14	155
QEVTAEDGT	<u>1170</u>	5207	31081	3122	7886	66	1843
CEKCSKPCA	<u>1171</u>	3740	27386	2703	19957	342	8007
MEHLREVRA	<u>1172</u>	233	44754	386	38	3.2	19
REVRVAVTSA	<u>1173</u>	626	427	0.71	3160	0.18	9.3
QEFAGCKKI	<u>1174</u>	1120	736	131	81	44	2684
EEITGYLYI	<u>1175</u>	86	906	916	12	121	94
RELGSLAL	<u>1176</u>	359	3.7	0.85	457	0.97	2262
GEGLACHQL	<u>1177</u>	13766	187	88	112	11	340
QECVEECRV	<u>1178</u>	15799	8755	1664	7150	210	4542
VEECRVLQG	<u>1179</u>	1528	8947	7622	14202	305	20142
EECRVLQGL	<u>1180</u>	890	7076	2029	717	434	1185
AEQRASPLT	<u>1181</u>	346	874	183	103	1.8	10
QETELVEPL	<u>1182</u>	12	62	85	681	3.5	1232
VEPLTPSGA	<u>1183</u>	7321	>9638.55	11	8516	191	17037
TELRKVKVL	<u>1184</u>	1514	4698	54	2128	2.5	14147
GENVKIPVA	<u>1185</u>	10755	14510	7.5	20309	2.7	7.0
KEILDEAYV	<u>1186</u>	1358	62	146	6466	8.4	42
DEAYVMAGV	<u>1187</u>	58	5327	1245	8006	138	161

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Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
DETEYHADG	<u>1188</u>	159	>11940.3	>65384.62	>24403.18	1397	13353
LESILRRRF	<u>1189</u>	29	>11940.3	3475	4.7	101	12918
GERLPQPPI	<u>1190</u>	62	71	15	63	1.1	15
LEDDDMGDL	<u>1191</u>	191	556	351	947	900	6251
EEYLVPPQG	<u>1192</u>	66	10344	136	651	126	131
EEEAPRSPL	<u>1193</u>	902	4490	2881	342	362	307
EEAPRSPLA	<u>1194</u>	486	10707	4900	180	294	4.5
SEGAGSDVF	<u>1195</u>	74	5627	6525	69	192	6960
PEYVNQPDV	<u>1196</u>	831	3437	1581	1109	48	2536
PEYLTPQGG	<u>1197</u>	1456	18951	13860	6532	284	18990
PERGAPPST	<u>1198</u>	385	4744	7679	1116	178	7767
AENPEYLGL	<u>1199</u>	17	81	271	44	2.5	155
MELAAALCRWG	<u>1200</u>	102	8684	1840	5.7	135	408
LELTYLPTNA	<u>1201</u>	332	325	10.4	6428	3.1	24
QEVQGYVLIA	<u>1202</u>	61	772	64	1871	15	11
FEDNYALAVL	<u>1203</u>	321	6.2	48	2844	3.8	3095
TEILKGGVLI	<u>1204</u>	1021	241	294	24	21	7600
GESSEDCQSL	<u>1205</u>	138636	8.1	23	427	5.1	2491
SEDCQSLTRT	<u>1206</u>	335	8550	11529	518	2857	4726
CELHCPALVT	<u>1207</u>	80	>9248.55	65	933	18	477
MEHLREVRAV	<u>1208</u>	72	20684	160	180	13	140
QEFAGCKKIF	<u>1209</u>	53	3686	12	4.0	3.6	115
FETLEEITGY	<u>1210</u>	671	53363	36302	262	1679	>28488.37
LEEITGYLYI	<u>1211</u>	143	914	2996	222	143	1488
RELGSGLALI	<u>1212</u>	4810	22	4.4	32	0.78	173
PEDECVGEGL	<u>1213</u>	1257	278	257	6331	49	24019
QECVEECRVL	<u>1214</u>	315	444	399	606	22	2863
VEECRVLQGL	<u>1215</u>	270	227	5815	237	189	16094
REYVNARHCL	<u>1216</u>	1327	39	4.8	106	0.97	126
PECQPQNGSV	<u>1217</u>	7962	35957	20374	12964	472	>28488.37
EEGACQPCPI	<u>1218</u>	119	40113	340	52	80	401
QETELVEPLT	<u>1219</u>	15	293	338	1619	13	288
VEPLTPSGAM	<u>1220</u>	4649	1667	584	4368	108	20167
KETELRKVKV	<u>1221</u>	11925	26700	68	2936	4.5	1603
TELRKVKVLG	<u>1222</u>	721	20312	601	3650	14	12816
GENVKIPVAI	<u>1223</u>	563	314	28	230	6.7	198
KEILDEAYVM	<u>1224</u>	0.14	10	153	35	7.5	234
DEAYVMAGVG	<u>1225</u>	122	203	154	4033	4102	218
DETEYHADGG	<u>1226</u>	613	45291	16801	3891	269	29025
TEYHADGGKV	<u>1227</u>	239	5246	2003	2911	15	1571
LESILRRRFT	<u>1228</u>	82	28476	1189	34	87	2251
REIPDLLEKG	<u>1229</u>	649	4493	814	1270	13	1977
SECRPRFREL	<u>1230</u>	80	307	18	11	0.20	25
RELVSEFSRM	<u>1231</u>	9.1	28	4.3	33	0.12	1726
NEDLGPA SPL	<u>1232</u>	107	281	150	40	6.0	231
AEEYLVPPQG	<u>1233</u>	723	66699	24424	417	479	127
EEYLVPPQGF	<u>1234</u>	2.1	26569	2551	6.9	11	73
SEEEAPRSPL	<u>1235</u>	151	155	217	37	8.4	84
EEEAPRSPLA	<u>1236</u>	6611	49549	38943	425	960	14
SETDGYVAPL	<u>1237</u>	94	214	184	386	2.4	302
PERGAPPSTF	<u>1238</u>	1062	14884	3437	6871	208	15700
PEYLGLDVPV	<u>1239</u>	613	352	35	1371	1.7	610

HLA-B44 SUPERTYPE							
Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
MELAAALCRWGL	<u>1240</u>	6.4	24	30	17	0.92	116
PETHLDMRLHL	<u>1241</u>	1322	700	2971	11534	70	4329
RELQLRSLTEI	<u>1242</u>	261	2.8	3.7	125	0.99	269
GESSEDCQSLT	<u>1243</u>	742	48	180	14386	40	2158
SEDCQSLTRTV	<u>1244</u>	101	4322	311	943	21	10
CELHCPALVTY	<u>1245</u>	12	3469	3198	140	89	2779
FESMPNPEGRY	<u>1246</u>	74	3666	3533	59	70	1394
CEKCSKPCARV	<u>1247</u>	1167	4103	2079	9594	101	1561
MEHLREVRAVT	<u>1248</u>	1064	3614	2207	795	111	74
REVRAVTSANI	<u>1249</u>	4491	17	30	1680	1.8	421
QEFAGCKKIFG	<u>1250</u>	211	314	477	37	2.1	138
FETLEEITGYL	<u>1251</u>	133	78	649	7490	42	2200
EEITGYLYISA	<u>1252</u>	0.94	1440	52	4.5	2.1	0.9
GEGLACHQLCA	<u>1253</u>	62	39	97	159	2.7	196
DEEGACQPCPI	<u>1254</u>	451	5517	7293	968	438	1323
AEQRASPLTSI	<u>1255</u>	467	19	58	5.1	2.5	11
TELVEPLTPSG	<u>1256</u>	601	2978	3703	>21052.63	269	14079
KETELRKVKVL	<u>1257</u>	9529	2973	1868	7136	71	12237
KEILDEAYVMA	<u>1258</u>	731	252	95	11514	64	123
LEDVRLVHRDL	<u>1259</u>	729	325	641	818	59	2382
WELMTFGAKPY	<u>1260</u>	13	509	778	24	75	1216
GERLPQPPICT	<u>1261</u>	12486	24270	23	9094	3.9	15
SECRPRFREL	<u>1262</u>	1996	3673	121	927	18	118
RELVSEFSRMA	<u>1263</u>	168	389	143	2613	3.5	32
AAEYLVPQQGF	<u>1264</u>	125	584	1831	21	99	268
EEYLVPQQGFF	<u>1265</u>	94	4291	1695	78	168	154
SEEEAPRSPLA	<u>1266</u>	1318	3604	5110	8550	158	27
SEGAGSDVFDG	<u>1267</u>	928	3751	5695	374	286	3008
SETDGYVAPLT	<u>1268</u>	66	125	224	1225	2.2	45
REGPLPAARPA	<u>1269</u>	157	543	78	32906	4.2	347
VENPEYLTPQG	<u>1270</u>	8386	56393	42593	17337	11	4188
PEYLTPQGGAA	<u>1271</u>	1724	41026	200	>17829.46	354	1382
AENPEYLGLDV	<u>1272</u>	11934	28	139	69	3.0	24
LELTYLPTNASL	<u>1273</u>	12	25	102	386	6.8	11
RELQLRSLTEIL	<u>1274</u>	5954	151	600	3778	1.1	1371
PEGRYTFGASCV	<u>1275</u>	4071	2.9	4.4	778		116
LEEITGYLYISA	<u>1276</u>	209	28	31	263	18	694
EEITGYLYISAW	<u>1277</u>	746	478	1800	252		1492
PEADQCACAHY	<u>1278</u>	901	4050	5127	213		463
TELVEPLTPSGA	<u>1279</u>	236	2059	59	2132		206
TEYHADGGKVPI	<u>1280</u>	680	22	4.4	2177		61
GERLPQPPICTI	<u>1281</u>	17769	162	3.9	292		2.5
AAEYLVPQQGFF	<u>1282</u>	144	228	45	16		13
PEGRYTFGASCVT	<u>1283</u>	5228	3793	737	1419	267	673
CEKCSKPCARVC	<u>1284</u>	701	>53333.33	406	302	44	1315
Y							
MEHLREVRAVTS	<u>1285</u>	70	669	72	144	18	12
A							
DECVGEGLACHQ	<u>1286</u>	464	2635	3668	2544	212	2063
L							
PECQPQNGSVTCF	<u>1287</u>	6293	381	5338	3564	375	>22374.43
RENTSPKANKEIL	<u>1288</u>	7750	3.7	77	>2540.03	3.9	1510
REIPDLLEKGERL	<u>1289</u>	7636	40	136	3050	16	2710

HLA-B44 SUPERTYPE							
Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
SEFSRMARDPQRF	<u>1290</u>	61	350	57	23	12	247
SEGAGSDVFDGD		5172	45	2059	1303	711	2458
L	<u>1291</u>						
GEFGGYGSV	<u>1292</u>	307	112	6.4	2335	534	40
LWQLNGRLEYTL						0.11	
KDR	<u>1293</u>						
SEFQAAI	<u>1294</u>	181	6830	779	2660	33	9597
SEYLQLV	<u>1295</u>	1375	7777	658	733	21	930
WEELSM	<u>1296</u>	1288	781	740	>28482.97	151	82009
GEPHISY	<u>1297</u>	8833	12272	6716	36116	272	>33333.33
LEARGEAL	<u>1298</u>	163	99	65	29495	2.9	31463
QEEEGPRM	<u>1299</u>	298	11598	1608	19255	118	6730
EEEGPRMF	<u>1300</u>	723	12281	32093	2406	213	943
VELVHFL	<u>1301</u>	5.0	69	31	3322	1.2	2427
AEMLESVL	<u>1302</u>	968	14	31	327	0.88	302
SEYLQLVF	<u>1303</u>	0.97	765	6.0	284	0.70	122
EEKIWEEL	<u>1304</u>	753	9084	2599	98976	104	171
LEARGEALG	<u>1305</u>	155	1161	3006	11018	24	2688
GEALGLVGA	<u>1306</u>	9529	2832	34	6134	2.2	17
QEEEGPRMF	<u>1307</u>	414	918	7747	237	409	2171
VELVHFLLL	<u>1308</u>	71	79	31	579	3.1	1129
REPVTKAEM	<u>1309</u>	60	373	284	896	4.5	832
SEYLQLVFG	<u>1310</u>	18	8890	421	271	19	113
PEEKIWEEL	<u>1311</u>	577	19449	3908	1029	235	17345
EELSMLEVF	<u>1312</u>	1.4	16436	252	22	2.8	1013
FEGREDSVF	<u>1313</u>	9.8	2366	348	221	13	3339
YEFLWGPRA	<u>1314</u>	5.3	249	5.2	2355	1.1	241
EEGLEARGEAL	<u>1315</u>	1077	3434	3227	216	302	30
LEARGEALGL	<u>1316</u>	81	184	277	2275	4.1	964
VEVTLGEVPA	<u>1317</u>	14	371	31	3801	0.52	15
EEGPRMFPDL	<u>1318</u>	128	4438	486	95	13	42
REPVTKAEM	<u>1319</u>	88	23	264	84	41	917
SEYLQLVFGI	<u>1320</u>	2.2	20	6.1	3.7	0.84	4.4
VEVVPISHLY	<u>1321</u>	20	11522	4385	13	1225	4885
EEKIWEELSM	<u>1322</u>	17	21450	477	46	19	107
WEELSMLEVF	<u>1323</u>	0.14	463	30	15	15	290
FEGREDSVFA	<u>1324</u>	178	>10062.89	4775	6879	192	503
QENYLEYRQV	<u>1325</u>	118	493	102	17	16	27
YEFLWGPRA	<u>1326</u>		8.5	0.97	130	0.72	753
GEPHISYPPL	<u>1327</u>	2612	7.0	2.9	1200	0.71	380
EEGLEARGEAL	<u>1328</u>	179	300	578	2630	19	1812
LEARGEALGLV	<u>1329</u>	158	198	345	>17829.46	13	1912
GEALGLVGAQA	<u>1330</u>	877	4293	52	3575	1.4	28
EEQQTASSSST	<u>1331</u>	752	4040	41162	5910	1552	134
VEVTLGEVPAA	<u>1332</u>	124	25216	919	>23469.39	44	1583
EEEGPRMFPDL	<u>1333</u>	1011	2646	3470	3273	131	209
SEFQAASIRKM	<u>1334</u>	7.0	345	107	88	1.2	161
VELVHFLLLKY	<u>1335</u>	52	550	294	1551	49	1790
LESVLRNCQDF	<u>1336</u>	64	5409	3458	209	76	15241
VEVVPISHLYI	<u>1337</u>	97	135	146	335	7.2	3788
IEGDCAPEEKI	<u>1338</u>	844	27827	32058	2627	486	183
EEKIWEELSM	<u>1339</u>	1641	4978	20625	1862	375	181

HLA-B44 SUPERTYPE							
Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
EELSMLEVFE	<u>1340</u>	1.5	24061	294	4.6	23	163
LEVFEGRSDV	<u>1341</u>	639	2624	367	>21296.3	46	29449
YEFWGPRLI	<u>1342</u>	5.2	4.1	2.8	92	0.59	450
EEQQTASSSTL	<u>1343</u>	7259	166	526	57	981	15
QEEEGPRMFPDL	<u>1344</u>	3595	394	1330	1643		120
SEFQAASIRKRV	<u>1345</u>	43	161	29	25		21
LESVLRNCQDF	<u>1346</u>	56	55	356	184	24	1993
VEVVPISHLYIL	<u>1347</u>	266	3.4	16	486	4.0	1182
EEGLEARGEALGL	<u>1348</u>	10416	1769	5143	196	118	1673
LEARGEALGLVGA	<u>1349</u>	347	20	48	2575	2.2	116
LESEFQAASIRKRV	<u>1350</u>	49	310	72	242	14	22
REPVTKAEMLESV	<u>1351</u>	5531	337	411	4546	21	1507
SEYLQLVFGIEVV	<u>1352</u>	9.7	23	4.5	144	5.4	6.6
IEVVEVVPISHLY	<u>1353</u>	79	162	245	52	125	106
VEVVPISHLYILV	<u>1354</u>	92	93	47	270	51	112
MEVDPIGHLY	<u>1355</u>	13	209	334	13	28	228
EEEGPSTF	<u>1356</u>	216	1008	435	3933	27	1819
AELVHFL	<u>1357</u>	120	71	6.8	1074	0.16	452
FEGREDSI	<u>1358</u>	927	718	127	7708	13	2291
QEAASSST	<u>1359</u>	1422	23469	1480	9593	41	110
AELVHFL	<u>1360</u>	160	25	3.1	33	0.94	141
AEMLGSVVG	<u>1361</u>	96	1899	109	27	1.6	11
EELSVLEVF	<u>1362</u>	7.3	10215	3314	61	12	2120
FEGREDSIL	<u>1363</u>	1091	51	439	1925	11	>27071.82
QEAASSSTL	<u>1364</u>	171	49	47	56	13	287
EEGPSTFPDL	<u>1365</u>	158	655	591	198	127	128
IELMEVDPIG	<u>1366</u>	194	6592	5325	222	>16306.95	7604
MEVDPIGHLY	<u>1367</u>	15	617	625	11	99	169
EKIWEELSV	<u>1368</u>	73	8947	79	396	17	17
WEELSVLEVF	<u>1369</u>	1.7	75	37	14	13	1701
FEGREDSILG	<u>1370</u>	229	940	4361	8534	172	20261
EEGPSTFPDL	<u>1371</u>	935	431	2120	2685	102	158
AELVHFL	<u>1372</u>	153	32	39	178	1.6	670
MEVDPIGHLYI	<u>1373</u>	9.8	34	16	64	0.91	95
REGDCAPEEKI	<u>1374</u>	973	2418	830	4038	42	146
EKIWEELSVL	<u>1375</u>	133	152	1255	1416	58	218
LEVFEGRSDI	<u>1376</u>	4745	206	512	20963	69	>31012.66
RERFEMF	<u>1377</u>	180	4079	1907	25488	108	20048
LEDSSGNL	<u>1378</u>	17736	782	362	42791	211	15946
GEYFTLQI	<u>1379</u>	7774	112	60	3511	1.0	261
VEPPLSQET	<u>1380</u>	8302	17052	20808	3186	236	29270
PENNVLSPL	<u>1381</u>	1150	1261	718	11174	8.8	>27071.82
DEAPRMPEA	<u>1382</u>	84	9092	4577	6448	98	10.0
HERCSDSDG	<u>1383</u>	1118	2367	38636	19328	208	13390
VEGNLRVEY	<u>1384</u>	832	12752	67730	142	2583	39059
VEYLDDRNT	<u>1385</u>	1442	36833	35854	10071	157	13503
LEDSSGNLL	<u>1386</u>	1140	43	2771	4656	43	26134
RELNEALEL	<u>1387</u>	3000	15	30	525	1.1	3337
NEALELKDA	<u>1388</u>	1925	3887	27585	4270	1582	129
LELKDAQAG	<u>1389</u>	451	18706	3659	17293	30	1989

HLA-B44 SUPERTYPE							
Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
MEEPQSDPSV	<u>1390</u>	12157	3802	16536	1927	816	175
VEPPLSQETF	<u>1391</u>	814	>37209.3	21732	406	525	>24019.61
QETFSDLWKL	<u>1392</u>	736	199	255	39	14	901
IEQWFTEDPG	<u>1393</u>	151	1250	2114	5595	142	197
DEAPRMPEAA	<u>1394</u>	121	3941	8444	2594	1037	100
HERCSDSDGL	<u>1395</u>	139	171	61	1468	6.0	1723
VEGNLRVEYL	<u>1396</u>	104	481	2565	1963	22	15189
VEYLDDRNTF	<u>1397</u>	0.94	501	37	32	1.4	3601
PEVGSDCTTI	<u>1398</u>	611	4552	248	2293	2046	22487
LEDSSGNLLG	<u>1399</u>	103	531	697	7905	153	19256
FEVRVCACPG	<u>1400</u>	64	2043	4.9	180	0.76	1872
TEENLRKKG	<u>1401</u>	74966	>37209.3	11858	>23589.74	315	30635
GEPHHELPPG	<u>1402</u>	108	3323	1888	11728	4.4	20
GEYFTLQIRG	<u>1403</u>	108	88	19	2452	3.9	157
RERFEMFREL	<u>1404</u>	83	29	17	17	0.34	422
FEMFRELNEA	<u>1405</u>	127	3207	223	952	2.0	208
QETFSDLWKLL	<u>1406</u>	4158	3366	740	631	168	1218
HERCSDSDGLA	<u>1407</u>	1408	4879	1915	>20956.72	96	186
YEPPEVGSDCT	<u>1408</u>	16872	4529	125	13349	12712	16034
HELPPGSTKRA	<u>1409</u>	6034	3974	3255	47077	189	1472
FEMFRELNEAL	<u>1410</u>	475	17	8.8	748	1.1	1352
NEALELKDAQA	<u>1411</u>	742	6235	5071	>20956.72	949	53
TEDPGPDEAPRM	<u>1412</u>	888	327	893	2053	161	1676
GEPHHELPPGST	<u>1413</u>	6822	24342	4631	6581	252	169
DEAPRMPEAAP V	<u>1414</u>	427	>48484.85	7258	>2762.76	1376	19
YEPPEVGSDCTTI	<u>1415</u>	8796	2699	1540	>2740.54	253	>20000
RERRDNYV	<u>1416</u>	>73809.52	71554	62	>67647.06	>34517.77	34648
SEIDLILGY	<u>1417</u>	3.0	285	140	4.8	8.5	397
AEIPTRVNY	<u>1418</u>	1691	7826	5443	333	23	1286
AEMGKFKFSY	<u>1419</u>	1517	2941	622	146	28	283
DEIGVIDLY	<u>1420</u>	11	>114285.71	>77272.73	707	212	>49000
AEMGKFKYSF	<u>1421</u>	155	113	3.8	18	31	186
SEAIHTFQY	<u>1422</u>	25	2895	1802	18	16	1078
SEAIYTFQF	<u>1423</u>	5.7	967	39	4.8	20	293
AEGIVTGQY	<u>1424</u>	7176	6462	1528	255	12	418
HETTYNSI	<u>1425</u>	1644	251	336	616	23959	6608
GELSYLNV	<u>1426</u>	>24800	4856	100	19013	23735	784
YEDTGKTI	<u>1427</u>	13997	794	83	7911	2177	49000
YENDIEKKI	<u>1428</u>	30992	1156	145	1725	371	

TABLE 23

HLA-DQ SUPERTYPES						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
AAAKAAAAAYAA	<u>1429</u>	13	Artificial sequence			A
(44)YAAAAAAKAAA	<u>1430</u>	13	Artificial sequence			A
AAFAAAKTAAFA	<u>1431</u>	13	Artificial sequence			A
YAAFAAAKTAAFA	<u>1432</u>	14	Artificial sequence			A
YAAFAAAKTAAFA	<u>1433</u>	14	Artificial sequence			A
AHAHAHAHAHAHA A	<u>1434</u>	16	HA			A
VLERYLLEAKEAENI	<u>1435</u>	15	Human	EPO	11	
VPDTKVNIFYAWKRME	<u>1436</u>	15	Human	EPO	41	
WKRMEVGQQAVEVWQ	<u>1437</u>	15	Human	EPO	51	
VGQQAVEVWQGLALL	<u>1438</u>	15	Human	EPO	56	
VEVWQGLALLSEAVL	<u>1439</u>	15	Human	EPO	61	
GLALLSEAVLRGQAL	<u>1440</u>	15	Human	EPO	66	
SEAVLRGQALLVNSS	<u>1441</u>	15	Human	EPO	71	
RGQALLVNSSQPWEP	<u>1442</u>	15	Human	EPO	76	
LQLHVDKAVSGLRSL	<u>1443</u>	15	Human	EPO	91	
KEAISPPDAASAAPL	<u>1444</u>	15	Human	EPO	116	
PPDAASAAPLRTITA	<u>1445</u>	15	Human	EPO	121	
SAAPLRTITADTRK	<u>1446</u>	15	Human	EPO	126	
EAENITTGTAEHTSL	<u>1447</u>	15	Human	EPO	21	A
RLFDNASLRAHRLHQ	<u>1448</u>	15	Human	Growth hormone	8	
QLAFDTYQEFEEAYI	<u>1449</u>	15	Human	Growth hormone	22	
ISLLLIQSWLEPVQF	<u>1450</u>	15	Human	Growth hormone	78	
NSLVYGASDSNVYDL	<u>1451</u>	15	Human	Growth hormone	99	
SDSNVYDLLKDLEEG	<u>1452</u>	15	Human	Growth hormone	106	
KIFGSLAFLPESFDGDPA	<u>1453</u>	18	Human	Her2/neu	369	
CLKDRRNFDIPEEIK	<u>1454</u>	15	Human	IFN-B	31	
QLQQFQKEDAAVTIY	<u>1455</u>	15	Human	IFN-B	46	
QKEDAAVTIYEMLQN	<u>1456</u>	15	Human	IFN-B	51	
STGWNETIVENLLAN	<u>1457</u>	15	Human	IFN-B	76	
ETIVENLLANVYHQR	<u>1458</u>	15	Human	IFN-B	81	
KEDSHCAWTIVRVEI	<u>1459</u>	15	Human	IFN-B	136	
MSYNLLGFLQRSSNT	<u>1460</u>	15	Human	IFN-B	1	A
QHLCSHLVEALYLV	<u>1461</u>	15	Human	Insulin beta chain	4	
GSHLVEALYLVCGER	<u>1462</u>	15	Human	Insulin beta chain	8	
GSDLVEALYLVCGER	<u>1463</u>	15	Human	Insulin beta chain	8	A
VEALYLVCGERGFLY	<u>1464</u>	15	Human	Insulin	12	A

HLA-DQ SUPERTYPES						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
VEALYLV TGERGFFY		15	Human	beta chain Insulin	12	A
IDVWLGG LAENFLPY	<u>1465</u>	15	Human	beta chain thyroid	632	
IDVWLGG LAYNFLPY	<u>1466</u>	15	Human	perox thyroid	632	A
IDVWLGG LALNFLPY	<u>1467</u>	15	Human	perox thyroid	632	A
IDVWLGG LASNFLPY	<u>1468</u>	15	Human	perox thyroid	632	A
IDVWLGG LAKNFLPY	<u>1469</u>	15	Human	perox thyroid	632	A
IDVWLGG LADNFLPY	<u>1470</u>	15	Human	perox thyroid	632	A
IDVYLGG LAENFLPY	<u>1471</u>	15	Human	perox thyroid	632	A
IDVLLGG LAENFLPY	<u>1472</u>	15	Human	perox thyroid	632	A
IDVSLGG LAENFLPY	<u>1473</u>	15	Human	perox thyroid	632	A
IDVKLGG LAENFLPY	<u>1474</u>	15	Human	perox thyroid	632	A
IDVDLGG LAENFLPY	<u>1475</u>	15	Human	perox thyroid	632	A
IDVWLGG LAENYLPY	<u>1476</u>	15	Human	perox thyroid	632	A
IDVWLGG LAENVLPY	<u>1477</u>	15	Human	perox thyroid	632	A
IDVWLGG LAENSLPY	<u>1478</u>	15	Human	perox thyroid	632	A
IDVWLGG LAENKLPY	<u>1479</u>	15	Human	perox thyroid	632	A
IDVWLGG LAENDLPY	<u>1480</u>	15	Human	perox thyroid	632	A
IYVWLGG LAENFLPY	<u>1481</u>	15	Human	perox thyroid	632	A
ILVWLGG LAENFLPY	<u>1482</u>	15	Human	perox thyroid	632	A
ISVWLGG LAENFLPY	<u>1483</u>	15	Human	perox thyroid	632	A
IKVWLGG LAENFLPY	<u>1484</u>	15	Human	perox thyroid	632	A
IEVWLGG LAENFLPY	<u>1485</u>	15	Human	perox thyroid	632	A
IDVWLGG LAENFLPF	<u>1486</u>	15	Human	perox thyroid	632	A
IDVWLGG LAENFLPL	<u>1487</u>	15	Human	perox thyroid	632	A
IDVWLGG LAENFLPS	<u>1488</u>	15	Human	perox thyroid	632	A
IDVWLGG LAENFLPK	<u>1489</u>	15	Human	perox thyroid	632	A
IDVWLGG LAENFLPD	<u>1490</u>	15	Human	perox thyroid	632	A
	<u>1491</u>					

HLA-DQ SUPERTYPES						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
IDVWLGGGLAENFYYPY	<u>1492</u>	15	Human	perox thyroid	632	A
IDVWLGGGLAENFVPY	<u>1493</u>	15	Human	perox thyroid	632	A
IDVWLGGGLAENFSPY	<u>1494</u>	15	Human	perox thyroid	632	A
IDVWLGGGLAENFKPY	<u>1495</u>	15	Human	perox thyroid	632	A
IDVWLGGGLAENFDPY	<u>1496</u>	15	Human	perox thyroid	632	A
IDVWLGGGLAEYFLPY	<u>1497</u>	15	Human	perox thyroid	632	A
IDVWLGGGLAELFLPY	<u>1498</u>	15	Human	perox thyroid	632	A
IDVWLGGGLAESFLPY	<u>1499</u>	15	Human	perox thyroid	632	A
IDVWLGGGLAEKFLPY	<u>1500</u>	15	Human	perox thyroid	632	A
IDVWLGGGLAEDFLPY	<u>1501</u>	15	Human	perox thyroid	632	A
IDVWLGGGLAEQFLPY	<u>1502</u>	15	Human	perox thyroid	632	A
IDVWLGGGLYENFLPY	<u>1503</u>	15	Human	perox thyroid	632	A
IDVWLGGGLLENFLPY	<u>1504</u>	15	Human	perox thyroid	632	A
IDVWLGGGLSENFLPY	<u>1505</u>	15	Human	perox thyroid	632	A
IDVWLGGGLKENFLPY	<u>1506</u>	15	Human	perox thyroid	632	A
IDVWLGGGLDENFLPY	<u>1507</u>	15	Human	perox thyroid	632	A
IDVWLGGGYAENFLPY	<u>1508</u>	15	Human	perox thyroid	632	A
IDVWLGGVAENFLPY	<u>1509</u>	15	Human	perox thyroid	632	A
IDVWLGGSAENFLPY	<u>1510</u>	15	Human	perox thyroid	632	A
IDVWLGGKAENFLPY	<u>1511</u>	15	Human	perox thyroid	632	A
IDVWLGGDAENFLPY	<u>1512</u>	15	Human	perox thyroid	632	A
IDVWLGYLAENFLPY	<u>1513</u>	15	Human	perox thyroid	632	A
IDVWLGLLAENFLPY	<u>1514</u>	15	Human	perox thyroid	632	A
IDVWLGSLAENFLPY	<u>1515</u>	15	Human	perox thyroid	632	A
IDVWLKGKLAENFLPY	<u>1516</u>	15	Human	perox thyroid	632	A
IDVWLGDLAENFLPY	<u>1517</u>	15	Human	perox thyroid	632	A
IDVWLYGLAENFLPY	<u>1518</u>	15	Human	perox thyroid perox	632	A

HLA-DQ SUPERTYPES						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
IDVWLLGLAENFLPY	<u>1519</u>	15	Human	thyroid perox	632	A
IDVWLSGLAENFLPY	<u>1520</u>	15	Human	thyroid perox	632	A
IDVWLKGLAENFLPY	<u>1521</u>	15	Human	thyroid perox	632	A
IDVWLDGLAENFLPY	<u>1522</u>	15	Human	thyroid perox	632	A
IDVWYGGLAENFLPY	<u>1523</u>	15	Human	thyroid perox	632	A
IDVWVGGLAENFLPY	<u>1524</u>	15	Human	thyroid perox	632	A
IDVWSGGLAENFLPY	<u>1525</u>	15	Human	thyroid perox	632	A
IDVWKGGLAENFLPY	<u>1526</u>	15	Human	thyroid perox	632	A
IDVWDGGLAENFLPY	<u>1527</u>	15	Human	thyroid perox	632	A
IDYWLGGGLAENFLPY	<u>1528</u>	15	Human	thyroid perox	632	A
IDLWLGGGLAENFLPY	<u>1529</u>	15	Human	thyroid perox	632	A
IDSWLGGGLAENFLPY	<u>1530</u>	15	Human	thyroid perox	632	A
IDKWLGGGLAENFLPY	<u>1531</u>	15	Human	thyroid perox	632	A
IDDWLGGGLAENFLPY	<u>1532</u>	15	Human	thyroid perox	632	A
IDVWLGGGLAENFLYY	<u>1533</u>	15	Human	thyroid perox	632	A
IDVWLGGGLAENFLLY	<u>1534</u>	15	Human	thyroid perox	632	A
IDVWLGGGLAENFLSY	<u>1535</u>	15	Human	thyroid perox	632	A
IDVWLGGGLAENFLKY	<u>1536</u>	15	Human	thyroid perox	632	A
IDVWLGGGLAENFLDY	<u>1537</u>	15	Human	thyroid perox	632	A
YDVWLGGGLAENFLPY	<u>1538</u>	15	Human	thyroid perox	632	A
LDVWLGGGLAENFLPY	<u>1539</u>	15	Human	thyroid perox	632	A
SDVWLGGGLAENFLPY	<u>1540</u>	15	Human	thyroid perox	632	A
KDVWLGGGLAENFLPY	<u>1541</u>	15	Human	thyroid perox	632	A
DDVWLGGGLAENFLPY	<u>1542</u>	15	Human	thyroid perox	632	A

TABLE 24

HLA-DQ SUPERTYPES				
Sequence	SEQ ID NO.	DQB1*030 1	DQB1*030 2	DQB1*020 1
AAAKAAAAAYAA	<u>1429</u>	424		
(44)YAAAAAAKAAA	<u>1430</u>	26		
AAFAAAKTAAFA	<u>1431</u>	49		
YAAFAAAKTAAFA	<u>1432</u>	36		
YAAFAAAKTAAFA	<u>1433</u>	39		
AHAAHAAHAAHAAHAA	<u>1434</u>	58		
VLERYLLEAKEAENI	<u>1435</u>	10932	309	5389
VPDTKVNIFYAWKRME	<u>1436</u>	730	>46666.67	>147058.82
WKRMEVGQQAVEVWQ	<u>1437</u>	13666	12146	159
VGQQAVEVWQGLALL	<u>1438</u>	1807	4407	838
VEVWQGLALLSEAVL	<u>1439</u>	19	14	98
GLALLSEAVLRGQAL	<u>1440</u>	107	16963	6742
SEAVLRGQALLVNSS	<u>1441</u>	55	36395	9755
RGQALLVNSSQPWEP	<u>1442</u>	302	14393	13362
LQLHVDKAVSGLRSL	<u>1443</u>	88	7842	7590
KEAISPPDAASAAPL	<u>1444</u>	458	960	7287
PPDAASAAPLRTITA	<u>1445</u>	20	3869	3631
SAAPLRTITADTFRK	<u>1446</u>	301	>46666.67	1100
EAENITTGTAEHTSL	<u>1447</u>	316	8300	
RLFDNASLRAHRLHQ	<u>1448</u>	996	>36206.9	11766
QLAFDTYQEFEEAYI	<u>1449</u>	>89285.71	673	35
ISLLLIQSWLEPVQF	<u>1450</u>	>89285.71	562	5234
NSLVYGASDSNVYDL	<u>1451</u>	14164	8337	731
SDSNVYDLLKDLEEG	<u>1452</u>	>89285.71	4136	503
KIFGSLAFLPESFDGDPA	<u>1453</u>	320		
CLKDRRNFDIPEEIK	<u>1454</u>	19365	208	774
QLQQFQKEDAAVTIY	<u>1455</u>	26205	579	2145
QKEDAAVTIYEMLQN	<u>1456</u>	515	153	1685
STGWNENIVENLLAN	<u>1457</u>	47081	5041	322
ETIVENLLANVYHQR	<u>1458</u>	>92592.59	>75000	344
KEDSHCAWTIVRVEI	<u>1459</u>	4102	2123	465
MSYNLLGFLQRSSNT	<u>1460</u>	724	>51219.51	
QHLGSHLVEALYLV	<u>1461</u>	2553	8413	359
GSHLVEALYLVCGER	<u>1462</u>	>89285.71	2491	677
GSDLVEALYLVCGER	<u>1463</u>	>89285.71	806	
VEALYLVCGERGFLY	<u>1464</u>	27334	514	
VEALYLVGTGERGFFY	<u>1465</u>	20021	564	
IDVWLGGLAENFLPY	<u>1466</u>	204	138	13
IDVWLGGLAYNFLPY	<u>1467</u>	85	358	63
IDVWLGGGLALNFLPY	<u>1468</u>	49	457	52
IDVWLGGGLASNFLPY	<u>1469</u>	175	1251	40
IDVWLGGGLAKNFLPY	<u>1470</u>	170	10247	>4166.67
IDVWLGGGLADNFLPY	<u>1471</u>	296	1762	12
IDVYLGGLAENFLPY	<u>1472</u>	161	186	30

HLA-DQ SUPERTYPES				
Sequence	SEQ ID NO.	DQB1*030 1	DQB1*030 2	DQB1*020 1
IDVLLGGLAENFLPY	<u>1473</u>	166	437	27
IDVSLGGLAENFLPY	<u>1474</u>	188	277	48
IDVKLGGLAENFLPY	<u>1475</u>	724	5511	41
IDVDLGGLAENFLPY	<u>1476</u>	218	73	17
IDVWLGGGLAENYLPY	<u>1477</u>	223	110	19
IDVWLGGGLAENVLPY	<u>1478</u>	84	82	15
IDVWLGGGLAENSLPY	<u>1479</u>	116	125	25
IDVWLGGGLAENKLPY	<u>1480</u>	353	5189	51
IDVWLGGGLAENDLPY	<u>1481</u>	240	60	22
IYVWLGGGLAENFLPY	<u>1482</u>	170	237	13
ILVWLGGGLAENFLPY	<u>1483</u>	216	147	10.0
ISVWLGGGLAENFLPY	<u>1484</u>	132	286	18
IKVWLGGGLAENFLPY	<u>1485</u>	180	220	37
IEVWLGGGLAENFLPY	<u>1486</u>	158	145	23
IDVWLGGGLAENFLPF	<u>1487</u>	111	177	3.6
IDVWLGGGLAENFLPL	<u>1488</u>	182	114	17
IDVWLGGGLAENFLPS	<u>1489</u>	134	249	27
IDVWLGGGLAENFLPK	<u>1490</u>	261	231	23
IDVWLGGGLAENFLPD	<u>1491</u>	115	91	20
IDVWLGGGLAENFYYPY	<u>1492</u>	324	203	37
IDVWLGGGLAENFVPY	<u>1493</u>	346	272	12
IDVWLGGGLAENFSPY	<u>1494</u>	131	193	47
IDVWLGGGLAENFKPY	<u>1495</u>	195	262	310
IDVWLGGGLAENFDPY	<u>1496</u>	364	90	32
IDVWLGGGLAEYFLPY	<u>1497</u>	151	88	14
IDVWLGGGLAELFLPY	<u>1498</u>	107	81	22
IDVWLGGGLAESFLPY	<u>1499</u>	60	64	49
IDVWLGGGLAEKFLPY	<u>1500</u>	68	112	66
IDVWLGGGLAEDFLPY	<u>1501</u>	357	120	23
IDVWLGGGLAEQFLPY	<u>1502</u>	167	123	9.7
IDVWLGGGLYENFLPY	<u>1503</u>	912	697	6.4
IDVWLGGGLLENFLPY	<u>1504</u>	810	1734	58
IDVWLGGGLSENFLPY	<u>1505</u>	242	1348	37
IDVWLGGGLKENFLPY	<u>1506</u>	15907	>2800	25
IDVWLGGGLDENFLPY	<u>1507</u>	>19230.77	637	18
IDVWLGGGYAENFLPY	<u>1508</u>	900	492	39
IDVWLGGGVAENFLPY	<u>1509</u>	982	327	75
IDVWLGGGSAENFLPY	<u>1510</u>	427	755	166
IDVWLGGGKAENFLPY	<u>1511</u>	517	633	398
IDVWLGGGDAENFLPY	<u>1512</u>	11114	2074	11
IDVWLGYLAENFLPY	<u>1513</u>	15215	1121	31
IDVWLGLLAENFLPY	<u>1514</u>	2986	180	39
IDVWLGLSLAENFLPY	<u>1515</u>	654	278	72
IDVWLGLKLAENFLPY	<u>1516</u>	2333	20023	81
IDVWLGLDLAENFLPY	<u>1517</u>	>44642.86	370	18
IDVWLGLYLAENFLPY	<u>1518</u>	2171	442	18

HLA-DQ SUPERTYPES				
Sequence	SEQ ID NO.	DQB1*030 1	DQB1*030 2	DQB1*020 1
IDVWLLGLAENFLPY	<u>1519</u>	4903	455	47
IDVWLSGLAENFLPY	<u>1520</u>	3043	373	98
IDVWLKGLAENFLPY	<u>1521</u>	41667	1115	55
IDVWLDGLAENFLPY	<u>1522</u>	13325	357	43
IDVWYGGLAENFLPY	<u>1523</u>	375	224	43
IDVWVGGLAENFLPY	<u>1524</u>	128	158	14
IDVWSGGLAENFLPY	<u>1525</u>	451	128	15
IDVWKGGLAENFLPY	<u>1526</u>	256	346	41
IDVWDGGLAENFLPY	<u>1527</u>	2086	299	112
IDYWLGGGLAENFLPY	<u>1528</u>	503	342	49
IDLWLGGGLAENFLPY	<u>1529</u>	1292	661	25
IDSWLGGGLAENFLPY	<u>1530</u>	508	276	35
IDKWLGGGLAENFLPY	<u>1531</u>	579	534	62
IDDWLGGGLAENFLPY	<u>1532</u>	219	101	85
IDVWLGGGLAENFLYY	<u>1533</u>	341	387	154
IDVWLGGGLAENFLLY	<u>1534</u>	649	491	52
IDVWLGGGLAENFLSY	<u>1535</u>	425	676	54
IDVWLGGGLAENFLKY	<u>1536</u>	2266	995	111
IDVWLGGGLAENFLDY	<u>1537</u>	371	149	49
YDVWLGGGLAENFLPY	<u>1538</u>	482	214	59
LDVWLGGGLAENFLPY	<u>1539</u>	180	216	29
SDVWLGGGLAENFLPY	<u>1540</u>	154	232	19
KDVWLGGGLAENFLPY	<u>1541</u>	348	254	54
DDVWLGGGLAENFLPY	<u>1542</u>	241	158	48

TABLE 25

HLA-DR SUPERTYPE					
Sequence	SEQ ID NO.	AA	Organism	Protein	Position Analog
AC- NPTKHKWEAAHVAE QLAA	<u>1543</u>	18	A2	MHC derived	Unknown
DDYVKQYTKQYTKQ NTLKK	<u>1544</u>	19	Artificial sequence		
AAAKAAAAAAYAA	<u>1545</u>	13	Artificial sequence		A
AC- AAAKAAAAAAYAA	<u>1546</u>	13	Artificial sequence		A
(20)AYA(20)A(20)A(20) K(20)A(20)	<u>1547</u>	13	Artificial sequence		A
AC- AAAKATAAAAYAA	<u>1548</u>	13	Artificial sequence		A
AC- AAAKAAAAAFAA	<u>1549</u>	13	Artificial sequence		A
AC- AAAKATAAAA(10)AA	<u>1550</u>	13	Artificial sequence		A
AC- AAAKATAAAA(23)AA	<u>1551</u>	13	Artificial sequence		A
AAKAAAAAAA(10)AA	<u>1552</u>	13	Artificial sequence		A
AAYAAAAATAKAAA	<u>1553</u>	13	Artificial sequence		A
AALAAAAAAKAAA	<u>1554</u>	13	Artificial sequence		A
AAEAAAAATAKAAA	<u>1555</u>	13	Artificial sequence		A
AAYJJAAAAKAAA	<u>1556</u>	13	Artificial sequence		A
AAYAAAAJJKAAA	<u>1557</u>	13	Artificial sequence		A
AFLRAAAAAAFAA	<u>1558</u>	13	Artificial sequence		A
AFLRQAAAAFAAY	<u>1559</u>	14	Artificial sequence		A
AAFAAAKTAAFA	<u>1560</u>	13	Artificial sequence		A
YAFAAAKTAAFA	<u>1561</u>	14	Artificial sequence		A
AALKATAAAAAA	<u>1562</u>	13	Artificial sequence		A
YAR(15)ASQTLKAKT	<u>1563</u>	14	Artificial sequence		
YARF(33)QTLKAKT	<u>1564</u>	14	Artificial sequence		
PKYFKQRILKFAT	<u>1565</u>	13	Artificial sequence		A
PKYFKQGFLKGAT	<u>1566</u>	13	Artificial sequence		A
PKYGKQIDLKGAT	<u>1567</u>	13	Artificial sequence		A
AAFFFFFGGGGA	<u>1568</u>	13	Artificial sequence		
AADFFFFFFFDA	<u>1569</u>	13	Artificial sequence		
AAKGKIGFGIFA	<u>1570</u>	13	Artificial sequence		
AAFIFIGGGKIKA	<u>1571</u>	13	Artificial sequence		
AAKIFIGFFIDGA	<u>1572</u>	13	Artificial sequence		

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
AAFIGFGKIKFIA	<u>1573</u>	13	Artificial sequence			
AAKIGFGIKIGFA	<u>1574</u>	13	Artificial sequence			
AAFKIGKFGIFFA	<u>1575</u>	13	Artificial sequence			
AADDDDDDDDDDA	<u>1576</u>	13	Artificial sequence			
(43)AAIGFFFFKKGIA	<u>1577</u>	14	Artificial sequence			
(43)AAFFGIFKIGKFA	<u>1578</u>	14	Artificial sequence			
(43)AADFGIFIDFIIA	<u>1579</u>	14	Artificial sequence			
(43)AAIGGIFIFKKDA	<u>1580</u>	14	Artificial sequence			
(43)AAFIGFGKIKFIA	<u>1581</u>	13	Artificial sequence			
(43)AAKIGFGIKIGFA	<u>1582</u>	13	Artificial sequence			
(43)AAFKIGKFGIFFA	<u>1583</u>	13	Artificial sequence			
AAAKAAAAAAAAAF	<u>1584</u>	13	Artificial sequence			
AAAKAAAAAAAAFA	<u>1585</u>	13	Artificial sequence			
AAAKAAAAAAFAA	<u>1586</u>	13	Artificial sequence			
AAAKAAAAFAAAA	<u>1587</u>	13	Artificial sequence			
FAAAAAAAAAAAAA	<u>1588</u>	13	Artificial sequence			
AAAAAAAAAAAAAN	<u>1589</u>	13	Artificial sequence			
AAAAAAAAAAAAANA	<u>1590</u>	13	Artificial sequence			
AAANAAAAAAAAAAA	<u>1591</u>	13	Artificial sequence			
AAAAAAAAAAAAAAS	<u>1592</u>	13	Artificial sequence			
AAAAASAAAAAAA	<u>1593</u>	13	Artificial sequence			
ASAAAAAAAAAAAA	<u>1594</u>	13	Artificial sequence			
AFAAAKTAA	<u>1595</u>	9	Artificial sequence			
YARFLALTTLRARA	<u>1596</u>	14	Artificial sequence			A
YAR(15A)SQTTLKAKT	<u>1597</u>	14	Artificial sequence			A
YAR(15A)RQTTLKAA	<u>1598</u>	14	Artificial sequence			A
A	<u>1599</u>	11	Artificial sequence			A
(15A)RQTTLKAAA	<u>1600</u>	11	Artificial sequence			A
(16A)RQTTLKAAA	<u>1601</u>	10	Artificial sequence			
(46)AAKTAAAF	<u>1602</u>	10	Artificial sequence			
(39)AAAAATKAAA	<u>1603</u>	11	Artificial sequence			
(52)AAAAATKAAAA						

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
(55)AAAATKAAAA	<u>1604</u>	11	Artificial sequence			
A(14)AAAKTAAA	<u>1605</u>	10	Artificial sequence			
AA(14)A(35)ATKAAA A	<u>1606</u>	12	Artificial sequence			
AA(14)AA(36)TKAAA A	<u>1607</u>	12	Artificial sequence			
AFAAAKTAA(72)	<u>1608</u>	10	Artificial sequence			
(49)AAAKT(64)AAA	<u>1609</u>	10	Artificial sequence			
(49)AAAKTA(64)AA	<u>1610</u>	10	Artificial sequence			
HQAISPRTLNGPGPGS PAIF	<u>1611</u>	20	Artificial sequence			
YAAFAAAKTAAAF	<u>1612</u>	14	Artificial sequence			
TEGRCLHYTVDKSKP K	<u>1613</u>	16	Bee Venom		103	
AWVAWRNRCK	<u>1614</u>	0	Chicken	HEL	107	
IVSDGNGMNAWVAW RNRC	<u>1615</u>	18	Chicken	HEL	98	
PHHTALRQAILSWGE LMTLA	<u>1616</u>	20	DPw4 binder			
WMYYHGQRHSDEHH H	<u>1617</u>	15	EBV	LMP	183	
YIVMSDWTGGA	<u>1618</u>	15	EBV	LMP	41	
AHAHAHAHAHAH AA	<u>1619</u>	16	HA			A
MDIDPYKEFGATVEL LSFLPSDFFP	<u>1620</u>	25	HBV	core	1	
GMLPVCPLIPGSSTTS TGP	<u>1621</u>	19	HBV	env	102	
LGFFPDHQLDPAFRA NT	<u>1622</u>	17	HBV	env	11	
GYKVLVLNPSV	<u>1623</u>	11	HCV	NS3	1248	
LMAFTAAVTS	<u>1624</u>	10	HCV	NS4	1790	
TFALWRVSAEY	<u>1625</u>	12	HCV	NS5	2079	
ALWRVSAEY	<u>1626</u>	10	HCV	NS5	2081	
EEYVEIRQVGDFH	<u>1627</u>	13	HCV	NS5	2088	
VGGVYLLPRRGPRLG V	<u>1628</u>	16	HCV			
VGGAYLLPRRGPRLG V	<u>1629</u>	16	HCV			A
VGGVALLPRRGPRLG V	<u>1630</u>	16	HCV			A
VGGVYALPRRGPRLG V	<u>1631</u>	16	HCV			A
VGGVYLAPRRGPRLG V	<u>1632</u>	16	HCV			A
VGGVYLLARRGPRLG V	<u>1633</u>	16	HCV			A
VGGVYLLPARGPRLG V	<u>1634</u>	16	HCV			A
VGGVYLLRRAGPRLG V	<u>1635</u>	16	HCV			A
GAPLGGAARALAHGV	<u>1636</u>	15	HCV			
GAALGGAARALAHG V	<u>1637</u>	15	HCV			A

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
GAPLAGAARALAHGV	<u>1638</u>	15	HCV			A
GAPLGAAARALAHGV	<u>1639</u>	15	HCV			A
GAPLGGLARALAHGV	<u>1640</u>	15	HCV			A
GAPLGGAALRALAHGV	<u>1641</u>	15	HCV			A
GAPLGGA AAAALAHG V	<u>1642</u>	15	HCV			A
GAPLGGAARLLAHGV	<u>1643</u>	15	HCV			A
GAPLGGAARAAAAG V	<u>1644</u>	15	HCV			A
GAPLGGAARALAAGV	<u>1645</u>	15	HCV			A
FPDWQNYTPGPGTRF	<u>1646</u>	15	HIV	NEF	200	
RFPLTFGWCFKLVPV	<u>1647</u>	15	HIV	NEF	216	
RQDILDLWVYHTQGY	<u>1648</u>	15	HIV	NEF	182	
RQEILDLWVYHTQGF	<u>1649</u>	15	HIV	NEF	182	
LSHFLKEKGGLEGLI	<u>1650</u>	15	HIV	NEF	114	
LSFFLKEKGGLDGLI	<u>1651</u>	15	HIV	NEF	114	
LEPWNHPGSQPKTAC T	<u>1652</u>	16	HIV	TAT	11	
QVCFITKGLGISYGR	<u>1653</u>	15	HIV	TAT	38	
QLCFLKKGLGISYGR	<u>1654</u>	15	HIV	TAT	38	
PPEESFRFGEEKTPS	<u>1655</u>	16	HIV1	gp	81	
CIVYRDGNPYAVCDK	<u>1656</u>	15	HPV	E6	58	
HYCYSLYGTTLEQQY	<u>1657</u>	15	HPV	E6	85	
CYSLYGTTLEQQYNK	<u>1658</u>	15	HPV	E6	87	
NTSLQDIEITCVYCK	<u>1659</u>	15	HPV	E6	22	
VFEFAFKDLFVVYRD	<u>1660</u>	15	HPV	E6	44	
EFAFKDLFVVYRDSI	<u>1661</u>	15	HPV	E6	46	
DLFVVYRDSIPHAAC	<u>1662</u>	15	HPV	E6	51	
FVVYRDSIPHAACHK	<u>1663</u>	15	HPV	E6	53	
NTGLYNLLIRCLRCQ	<u>1664</u>	15	HPV	E6	95	
IRCLRCQKPLNPAEK	<u>1665</u>	15	HPV	E6	103	
PRKLHELSSALEIPY	<u>1666</u>	15	HPV	E6	9	
EIPYDELRLNLCVYCK	<u>1667</u>	15	HPV	E6	20	
TEVLDFAFDTLTIVY	<u>1668</u>	15	HPV	E6	40	
VLDFAFDTLTIVYRD	<u>1669</u>	15	HPV	E6	42	
DFAFTDLTIVYRDDT	<u>1670</u>	15	HPV	E6	44	
TIVYRDDTPHGVCTK	<u>1671</u>	15	HPV	E6	51	
WYRYSVYGTTLEKLT	<u>1672</u>	15	HPV	E6	78	
ETTIHNIELQCVECK	<u>1673</u>	15	HPV	E6	20	
SEVYDFAFADLTVVY	<u>1674</u>	15	HPV	E6	40	
VYDFAFADLTVVYRE	<u>1675</u>	15	HPV	E6	42	
DFAFADLTVVYREGN	<u>1676</u>	15	HPV	E6	44	
TVVYREGNPFGICKL	<u>1677</u>	15	HPV	E6	51	
GNPFGICKLCLRFLS	<u>1678</u>	15	HPV	E6	57	
NYSVYGNTLEQTVKK	<u>1679</u>	15	HPV	E6	80	
KKPLNEILIRCIICQ	<u>1680</u>	15	HPV	E6	93	
NEILIRCIICQRPLC	<u>1681</u>	15	HPV	E6	97	
IRCIICQRPLCPQEK	<u>1682</u>	15	HPV	E6	101	

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
CIVYRDCIAYAACHK	<u>1683</u>	15	HPV	E6	53	
NTELYNLLIRCLRCQ	<u>1684</u>	15	HPV	E6	95	
IRCLRCQKPLNPAEK	<u>1685</u>	15	HPV	E6	103	
REVKFLFTDLRIVY	<u>1686</u>	15	HPV	E6	40	
RIVYRDNNPYGVCIM	<u>1687</u>	15	HPV	E6	51	
NNPYGVCIMCLRFLS	<u>1688</u>	15	HPV	E6	57	
EERVKKPLSEITIRC	<u>1689</u>	15	HPV	E6	89	
IRCICQTPLCPEEK	<u>1690</u>	15	HPV	E6	101	
EIPLIDLRRLSCVYCK	<u>1691</u>	15	HPV	E6	23	
SCVYCKKELTRAENVY	<u>1692</u>	15	HPV	E6	32	
VCLLFYSKVRKYRYY	<u>1693</u>	15	HPV	E6	68	
YYDYSVYGATLESIT	<u>1694</u>	15	HPV	E6	81	
IRCYRCQSPLTPEEK	<u>1695</u>	15	HPV	E6	104	
VYDFVFADLRIVYRD	<u>1696</u>	15	HPV	E6	42	
DFVFADLRIVYRDGN	<u>1697</u>	15	HPV	E6	44	
RIVYRDGNPFVAVCKV	<u>1698</u>	15	HPV	E6	51	
GNPFVAVCKVCLRLLS	<u>1699</u>	15	HPV	E6	57	
KKCLNEILIRCIICQ	<u>1700</u>	15	HPV	E6	93	
NEILIRCIICQRPLC	<u>1701</u>	15	HPV	E6	97	
RTAMFQDPQERPRKL	<u>1702</u>	15	HPV	E6	5	
LFVVYRDSIPHAACH	<u>1703</u>	15	HPV	E6	52	
LTIVYRDDTPHGVCT	<u>1704</u>	15	HPV	E6	50	
LCIVYRDCIAYAAACH	<u>1705</u>	15	HPV	E6	52	
YKFLFTDLRIVYRDN	<u>1706</u>	15	HPV	E6	43	
YNFACTELKLIVYRDD	<u>1707</u>	15	HPV	E6	46	
LKLVYRDDFPYAVCR	<u>1708</u>	15	HPV	E6	53	
YDFVFADLRIVYRDG	<u>1709</u>	15	HPV	E6	43	
LRIVYRDGNPFVAVCK	<u>1710</u>	15	HPV	E6	50	
HEYMLDLQPETTDLY	<u>1711</u>	15	HPV	E7	9	
TLRLCVQSTHVDIRT	<u>1712</u>	15	HPV	E7	64	
IRTLEDLLMGTLGIV	<u>1713</u>	15	HPV	E7	76	
LEDLLMGTLGIVCPI	<u>1714</u>	15	HPV	E7	79	
DLLMGTLGIVCPICS	<u>1715</u>	15	HPV	E7	81	
KATLQDIVLHLEPQN	<u>1716</u>	15	HPV	E7	5	
IDGVNHQHLPARRAE	<u>1717</u>	15	HPV	E7	41	
LRAFQQLFLNTLSFV	<u>1718</u>	15	HPV	E7	83	
FQQLFLNTLSFVCPW	<u>1719</u>	15	HPV	E7	86	
QDYVLDLQPEATDLH	<u>1720</u>	15	HPV	E7	9	
DIRILQELLMGSFGI	<u>1721</u>	15	HPV	E7	75	
IRILQELLMGSFGIV	<u>1722</u>	15	HPV	E7	76	
ELLMGSFGIVCPNCS	<u>1723</u>	15	HPV	E7	81	
KEYVLDLYPEPTDLY	<u>1724</u>	15	HPV	E7	9	
LRTIQQLMGTVNIV	<u>1725</u>	15	HPV	E7	76	
IQQLMGTVNIVCPT	<u>1726</u>	15	HPV	E7	79	
QQLMGTVNIVCPTCA	<u>1727</u>	15	HPV	E7	81	
RETLQEIVLHLEPQN	<u>1728</u>	15	HPV	E7	5	

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
LRTLQQLFLSTLSFV	<u>1729</u>	15	HPV	E7	84	
LQQLFLSTLSFVCPW	<u>1730</u>	15	HPV	E7	87	
KDYILDLQPETTDLH	<u>1731</u>	15	HPV	E7	9	
LRTLQQMLLGTLQVV	<u>1732</u>	15	HPV	E7	78	
LQQMLLGTLQVVCPG	<u>1733</u>	15	HPV	E7	81	
QMLLGTLQVVCPGCA	<u>1734</u>	15	HPV	E7	83	
VPTLQDVVLELTPQT	<u>1735</u>	15	HPV	E7	5	
LQDVVLELTPQTEID	<u>1736</u>	15	HPV	E7	8	
QDVVLELTPQTEIDL	<u>1737</u>	15	HPV	E7	9	
CKFVVQLDIQSTKED	<u>1738</u>	15	HPV	E7	68	
VVQLDIQSTKEDLRV	<u>1739</u>	15	HPV	E7	71	
DLRVVQQLLMGALTV	<u>1740</u>	15	HPV	E7	82	
LRVVQQLMGALTVT	<u>1741</u>	15	HPV	E7	83	
VQQLMGALTVTCPL	<u>1742</u>	15	HPV	E7	86	
QQLMGALTVTCPLC	<u>1743</u>	15	HPV	E7	87	
QLMGALTVTCPLCA	<u>1744</u>	15	HPV	E7	88	
REYILDLHPEPTDLF	<u>1745</u>	15	HPV	E7	9	
TCCYTCGTTVRLCIN	<u>1746</u>	15	HPV	E7	57	
VRTLQQLMGCTIV	<u>1747</u>	15	HPV	E7	77	
LQQLMGCTIVCPS	<u>1748</u>	15	HPV	E7	80	
MLDLQPETTDLYCYE	<u>1749</u>	15	HPV	E7	12	
VLDLYPEPTDLYCYE	<u>1750</u>	15	HPV	E7	12	
LREYILDLHPEPTDL	<u>1751</u>	15	HPV	E7	8	
HIEFTPTRTDTYACRV	<u>1752</u>	16	Human	B2-μglobulin	67	
LWWWNNESLPVSPRL	<u>1753</u>	15	Human	CEA	177	A
YEEYVRFDSVDVGE	<u>1754</u>	13	Human	DRB and CD4 peptide		
EEYVRFDSVDVGE	<u>1755</u>	12	Human	DRB and CD4 peptide		
APPRLICDSRVLERY	<u>1756</u>	15	Human	EPO	1	
ICDSRVLERYLLEAK	<u>1757</u>	15	Human	EPO	6	
VLERYLLEAKEAENI	<u>1758</u>	15	Human	EPO	11	
EHCSLNENITVPDTK	<u>1759</u>	15	Human	EPO	31	
NENITVPDTKVNFYA	<u>1760</u>	15	Human	EPO	36	
VPDTKVNFYAWKRM	<u>1761</u>	15	Human	EPO	41	
E	<u>1761</u>					
VNFYAWKRMEVGQQ	<u>1762</u>	15	Human	EPO	46	
A	<u>1762</u>					
WKRMEVGQQAVEV	<u>1763</u>	15	Human	EPO	51	
WQ	<u>1763</u>					
VGQQAVEVWQGLAL	<u>1764</u>	15	Human	EPO	56	
L	<u>1764</u>					
VEVWQGLALLSEAVL	<u>1765</u>	15	Human	EPO	61	
GLALLSEAVLRGQAL	<u>1766</u>	15	Human	EPO	66	
SEAVLRGQALLVNSS	<u>1767</u>	15	Human	EPO	71	
RGQALLVNSSQPWEP	<u>1768</u>	15	Human	EPO	76	
LVNSSQPWEPLQLHV	<u>1769</u>	15	Human	EPO	81	
QPWEPLQLHVDKAVS	<u>1770</u>	15	Human	EPO	86	
LQLHVDKAVSGLRSL	<u>1771</u>	15	Human	EPO	91	

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
DKAVSGLRSLTTLLR	<u>1772</u>	15	Human	EPO	96	
GLRSLTTLLRALGAQ	<u>1773</u>	15	Human	EPO	101	
TTLRLALGAQKEAIS	<u>1774</u>	15	Human	EPO	106	
ALGAQKEAISPPDAA	<u>1775</u>	15	Human	EPO	111	
KEAISPPDAASAAPL	<u>1776</u>	15	Human	EPO	116	
PPDAASAAPLRTITA	<u>1777</u>	15	Human	EPO	121	
SAAPLRTITADTFRK	<u>1778</u>	15	Human	EPO	126	
RTITADTFRKLFRVY	<u>1779</u>	15	Human	EPO	131	
DTFRKLFRVYSNFLR	<u>1780</u>	15	Human	EPO	136	
LFRVYSNFLRGKCLKL	<u>1781</u>	15	Human	EPO	141	
SNFLRGKCLKLYTGEA	<u>1782</u>	15	Human	EPO	146	
KLKLYTGEACRTGDR	<u>1783</u>	15	Human	EPO	152	
APRLITDSRVLERY	<u>1784</u>	15	Human	EPO	1	A
ITDSRVLERYLLEAK	<u>1785</u>	15	Human	EPO	6	A
EHTSLNENITVPDTK	<u>1786</u>	15	Human	EPO	31	A
KLKLYTGEATRTGDR	<u>1787</u>	15	Human	EPO	152	A
PQFRPQQPYPQ	<u>1788</u>	12	Human	gliadin		
PFRPQQPYPQ	<u>1789</u>	10	Human	gliadin		
PQFRPQQPYP	<u>1790</u>	11	Human	gliadin		
PQFRPQQP	<u>1791</u>	9	Human	gliadin		
KQFRPQQPYPQ	<u>1792</u>	12	Human	gliadin		
PKFRPQQPYPQ	<u>1793</u>	12	Human	gliadin		
PQPFKPQQPYPQ	<u>1794</u>	12	Human	gliadin		
PQFRKQQPYPQ	<u>1795</u>	12	Human	gliadin		
PQFRPQKPYPQ	<u>1796</u>	12	Human	gliadin		
PQFRPQQPKPQ	<u>1797</u>	12	Human	gliadin		
PQFRPQQPYKQ	<u>1798</u>	12	Human	gliadin		
PQFRPQQPYPK	<u>1799</u>	12	Human	gliadin		
QFLGQQQPFPPQ	<u>1800</u>	12	Human	gliadin		
FLGQQQPFPPQ	<u>1801</u>	11	Human	gliadin		
LGQQQPFPPQ	<u>1802</u>	10	Human	gliadin		
QFLGQQQPFPP	<u>1803</u>	11	Human	gliadin		
QFLGQQQPF	<u>1804</u>	9	Human	gliadin		
IRNLALQTLPAMCNV Y	<u>1805</u>	16	Human	gliadin		
NLALQTLPAMCNVY	<u>1806</u>	14	Human	gliadin		
LALQTLPAMCNVY	<u>1807</u>	13	Human	gliadin		
IRNLALQTLPAM	<u>1808</u>	12	Human	gliadin		
IRNLALQTLP	<u>1809</u>	10	Human	gliadin		
EGDAFELTVSCQGGL PK	<u>1810</u>	17	Human	gp100	506	
ESTGMTPEKVPVSEV MGT	<u>1811</u>	18	Human	gp100	370	
FPTIPLSRLFDNASL	<u>1812</u>	15	Human	Growth hormone	1	
RLFDNASLRAHRLHQ	<u>1813</u>	15	Human	Growth hormone	8	
LRAHRLHQLAFDTYQ	<u>1814</u>	15	Human	Growth hormone	15	

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
QLAFDTYQEFEEAYI	<u>1815</u>	15	Human	Growth hormone	22	
QEFEEAYIPKEQKYS	<u>1816</u>	15	Human	Growth hormone	29	
IPKEQKYSFLQNPQT	<u>1817</u>	15	Human	Growth hormone	36	
SFLQNPQTSLCFSES	<u>1818</u>	15	Human	Growth hormone	43	
TSLCFSESIPTPSNR	<u>1819</u>	15	Human	Growth hormone	50	
REETQQKSNLELLRI	<u>1820</u>	15	Human	Growth hormone	64	
SNLELLRISLLLIQS	<u>1821</u>	15	Human	Growth hormone	71	
ISLLLIQSWLEPVQF	<u>1822</u>	15	Human	Growth hormone	78	
SWLEPVQFLRSVFAN	<u>1823</u>	15	Human	Growth hormone	85	
FLRSVFANSLVYGAS	<u>1824</u>	15	Human	Growth hormone	92	
NSLVYGASDSNVYDL	<u>1825</u>	15	Human	Growth hormone	99	
SDSNVYDLLKDLEEG	<u>1826</u>	15	Human	Growth hormone	106	
GIQTLMGRLEDGSPR	<u>1827</u>	15	Human	Growth hormone	120	
RLEDGSPRTGQIFKQ	<u>1828</u>	15	Human	Growth hormone	127	
RTGQIFKQTYSKFDT	<u>1829</u>	15	Human	Growth hormone	134	
QTYSKFDTNSHNDDA	<u>1830</u>	15	Human	Growth hormone	141	
TNSHNDDALLKNYGL	<u>1831</u>	15	Human	Growth hormone	148	
ALLKNYGLLYCFRKD	<u>1832</u>	15	Human	Growth hormone	155	
DMDKVETFLRIVQCR	<u>1833</u>	15	Human	Growth hormone	169	
FLRIVQCRSVEGSCGF	<u>1834</u>	16	Human	Growth hormone	176	
FPTIPLSRLFDNAML	<u>1835</u>	15	Human	Growth hormone	1	A
RLFDNAMLRAHRLHQ	<u>1836</u>	15	Human	Growth hormone	8	A
QLAFDTYQEFEQNPQ	<u>1837</u>	15	Human	Growth hormone	22	A
SFLQNPQTSLCCFRK	<u>1838</u>	15	Human	Growth hormone	43	A
SNLELLRICLLLIQS	<u>1839</u>	15	Human	Growth hormone	71	A
ICLLLIQSWLEPVQF	<u>1840</u>	15	Human	Growth hormone	78	A
NSLVYGASDSNIYDL	<u>1841</u>	15	Human	Growth hormone	99	A
SDSNIYDLLKDLEEG	<u>1842</u>	15	Human	Growth hormone	106	A
DKVETFLRIVQCCGF	<u>1843</u>	15	Human	Growth hormone	169	A
SFLQNPQTSLTFSSES	<u>1844</u>	15	Human	Growth hormone	43	A
TSLTFSESIPTPSNR	<u>1845</u>	15	Human	Growth hormone	50	A

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
ALLKNYGLLYTFRKD	<u>1846</u>	15	Human	Growth hormone	155	A
LLYTFRKDMDKVETF	<u>1847</u>	15	Human	Growth hormone	162	A
DMDKVETFLRIVQTR	<u>1848</u>	15	Human	Growth hormone	169	A
FLRIVQTRSVEGSTGF	<u>1849</u>	16	Human	Growth hormone	176	A
HLDMLRHL YQGCQV V	<u>1850</u>	15	Human	Her2/neu	42	
RLRIVRG TQLFEDNYA L	<u>1851</u>	17	Human	Her2/neu	98	
GVGSPYVSRLLGICL	<u>1852</u>	15	Human	Her2/neu	776	
TLERPKTLSPGKNGV	<u>1853</u>	15	Human	Her2/neu	1166	
KIFGSLAFLPESFDGDP A	<u>1854</u>	18	Human	Her2/neu	369	
ELVSEFSRMARDPQ	<u>1855</u>	14	Human	Her2/neu	971	
GEALSTLVNRLKVG	<u>1856</u>	15	Human	HSP60	280	
AYVLLSEKKISSIQS	<u>1857</u>	15	Human	HSP60	242	
VASLLTTAEVVVTEI	<u>1858</u>	15	Human	HSP60	535	
KCEFQDAYVILLSEKK	<u>1859</u>	16	Human	HSP60	236	
ALSTLVNRLKVGLQ	<u>1860</u>	15	Human	HSP60	282	
MSYNLLGFLQRSSNC	<u>1861</u>	15	Human	IFN-B	1	
LGFLQRSSNCQCQKL	<u>1862</u>	15	Human	IFN-B	6	
RSSNCQCQKLLWQLN	<u>1863</u>	15	Human	IFN-B	11	
QCQKLLWQLNGRLEY	<u>1864</u>	15	Human	IFN-B	16	
LWQLNGRLEYCLKDR	<u>1865</u>	15	Human	IFN-B	21	
GRLEYCLKDRRNFDI	<u>1866</u>	15	Human	IFN-B	26	
RNFDIPEEIKQLQQF	<u>1867</u>	15	Human	IFN-B	36	
PEEIKQLQQFQKEDA	<u>1868</u>	15	Human	IFN-B	41	
QLQQFQKEDAAVTIY	<u>1869</u>	15	Human	IFN-B	46	
QKEDAAVTIYEMLQN	<u>1870</u>	15	Human	IFN-B	51	
AVTIYEMLQNIFAIF	<u>1871</u>	15	Human	IFN-B	56	
EMLQNIFAIFRQDSS	<u>1872</u>	15	Human	IFN-B	61	
IFAIFRQDSSSTGWN	<u>1873</u>	15	Human	IFN-B	66	
RQDSSSTGWNETIVE	<u>1874</u>	15	Human	IFN-B	71	
STGWNETIVENLLAN	<u>1875</u>	15	Human	IFN-B	76	
ETIVENLLANVYHQR	<u>1876</u>	15	Human	IFN-B	81	
NLLANVYHQRNHLKT	<u>1877</u>	15	Human	IFN-B	86	
VYHQRNHLKTVLEEK	<u>1878</u>	15	Human	IFN-B	91	
LEKEDFTRGKRMSSL	<u>1879</u>	15	Human	IFN-B	106	
FTRGKRMSSLHLKRY	<u>1880</u>	15	Human	IFN-B	111	
RMSSLHLKRYYGRIL	<u>1881</u>	15	Human	IFN-B	116	
HLKRYYGRILHYLKA	<u>1882</u>	15	Human	IFN-B	121	
YGRILHYLKAKEDSH	<u>1883</u>	15	Human	IFN-B	126	
HYLKAKEDSHCAWTI	<u>1884</u>	15	Human	IFN-B	131	
KEDSHCAWTIVRVEI	<u>1885</u>	15	Human	IFN-B	136	
CAWTIVRVEILRNFY	<u>1886</u>	15	Human	IFN-B	141	
VRVEILRNFYVINRL	<u>1887</u>	15	Human	IFN-B	146	
RNFYVINRLTGyLRN	<u>1888</u>	15	Human	IFN-B	152	

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
MSYNLLGFLQRSSNT	<u>1889</u>	15	Human	IFN-B	1	A
LGFLQRSSNTQTQKL	<u>1890</u>	15	Human	IFN-B	6	A
RSSNTQTQKLLWQLN	<u>1891</u>	15	Human	IFN-B	11	A
QTQKLLWQLNGRLEY	<u>1892</u>	15	Human	IFN-B	16	A
LWQLNGRLEYTLKDR	<u>1893</u>	15	Human	IFN-B	21	A
GRLEYTLKDRRNFDI	<u>1894</u>	15	Human	IFN-B	26	A
HYLKAKEDSHTAWTI	<u>1895</u>	15	Human	IFN-B	131	A
KEDSHTAWTIVRVEI	<u>1896</u>	15	Human	IFN-B	136	A
TAWTIVRVEILRNFY	<u>1897</u>	15	Human	IFN-B	141	A
LGFLQRSSNCQSQKL	<u>1898</u>	15	Human	IFN-B	6	A
RSSNCQSQKLLWQLN	<u>1899</u>	15	Human	IFN-B	11	A
QSQKLLWQLNGRLEY	<u>1900</u>	15	Human	IFN-B	16	A
GIVEQCCTSICSLYQ	<u>1901</u>	15	Human	Insulin alpha chain	1	
TSICSLYQLENYCN	<u>1902</u>	14	Human	Insulin alpha chain	8	
GILEQCCTSICSLYQ	<u>1903</u>	15	Human	Insulin alpha chain	1	A
GIVEQTTTSITSLYQ	<u>1904</u>	15	Human	Insulin alpha chain	1	A
EQTTSITSLYQLEN	<u>1905</u>	15	Human	Insulin alpha chain	4	A
TSICSLYQLENYCG	<u>1906</u>	14	Human	Insulin alpha chain	8	A
TSITSLYQLENYTN	<u>1907</u>	14	Human	Insulin alpha chain	8	A
TSITSLYQLENYTG	<u>1908</u>	14	Human	Insulin alpha chain	8	A
GIVEQCCCGSHLVEA	<u>1909</u>	15	Human	Insulin alpha- beta		A
SLYQLENYCCGERGF	<u>1910</u>	15	Human	Insulin alpha- beta		A
CCTSICSLYQLENYCC	<u>1911</u>	16	Human	Insulin alpha- beta		A
GSHLVEALYLVCN	<u>1912</u>	14	Human	Insulin alpha- beta		A
CCGSHLVEALYLVC	<u>1913</u>	15	Human	Insulin alpha- beta		A
FVNQHLCGSHLVEAL	<u>1914</u>	15	Human	Insulin beta chain	1	
QHLCGSHLVEALYLV	<u>1915</u>	15	Human	Insulin beta chain	4	
GSHLVEALYLVCGER	<u>1916</u>	15	Human	Insulin beta chain	8	
VEALYLVCGERGFFY	<u>1917</u>	15	Human	Insulin beta chain	12	
YLVCGERGFFYTPKT	<u>1918</u>	15	Human	Insulin beta chain	16	
FVNQHLCGSDLVEAL	<u>1919</u>	15	Human	Insulin beta chain	1	A
FVNQHLTGSHLVEAL	<u>1920</u>	15	Human	Insulin beta chain	1	A
QHLTGSHLVEALYLV	<u>1921</u>	15	Human	Insulin beta chain	4	A
GSHLVEALYLVGTGER	<u>1922</u>	15	Human	Insulin beta chain	8	A
VEALYLVCGERGSFY	<u>1923</u>	15	Human	Insulin beta chain	12	A

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
VEALYLVCGERGFLY	<u>1924</u>	15	Human	Insulin beta chain	12	A
VEALYLVLTGERGFFY	<u>1925</u>	15	Human	Insulin beta chain	12	A
YLVCGERGFLYTPKT	<u>1926</u>	15	Human	Insulin beta chain	16	A
YLVCGERGFFYTDKT	<u>1927</u>	15	Human	Insulin beta chain	16	A
YLVCGERGFFYTKPT	<u>1928</u>	15	Human	Insulin beta chain	16	A
YLVLTGERGFFYTPKT	<u>1929</u>	15	Human	Insulin beta chain	16	A
YLVLTGERGFFYTDKT	<u>1930</u>	15	Human	Insulin beta chain	16	A
YLVLTGERGFFYTKPT	<u>1931</u>	15	Human	Insulin beta chain	16	A
VCGERGFFYTPKTRR	<u>1932</u>	15	Human	Insulin beta chain	18	A
VTGERGFFYTPKTRR	<u>1933</u>	15	Human	Insulin beta chain	18	A
MWDLVLSIALSVGCT	<u>1934</u>	15	Human	Kallikrein2	1	
DLVLSIALSVGCTGA	<u>1935</u>	15	Human	Kallikrein2	3	
HPQWVLTAAHCLKK N	<u>1936</u>	15	Human	Kallikrein2	56	
QWVLTAAHCLKKNS Q	<u>1937</u>	15	Human	Kallikrein2	58	
GQRVPVSHSFPHPLY	<u>1938</u>	15	Human	Kallikrein2	87	
RVPVSHSFPHPLYNM	<u>1939</u>	15	Human	Kallikrein2	89	
PHPLYNMSLLKHQSL	<u>1940</u>	15	Human	Kallikrein2	97	
HPLYNMSLLKHQSLR	<u>1941</u>	15	Human	Kallikrein2	98	
NMSLLKHQSLRPDED	<u>1942</u>	15	Human	Kallikrein2	102	
SHDMLLRLSEPAKI	<u>1943</u>	15	Human	Kallikrein2	118	
HDLMLLRLSEPAKIT	<u>1944</u>	15	Human	Kallikrein2	119	
PEEFLRPRSLQCVSL	<u>1945</u>	15	Human	Kallikrein2	162	
PRSLQCVSLHLLSND	<u>1946</u>	15	Human	Kallikrein2	168	
NGVLQGITSWGPEPC	<u>1947</u>	15	Human	Kallikrein2	220	
KPAVYTKVVHYRKWI	<u>1948</u>	15	Human	Kallikrein2	239	
LHLLSNDM CARAYSE	<u>1949</u>	15	Human	Kallikrein2	176	
VGNWQYFFPVIFSKA	<u>1950</u>	15	Human	MAGE3	140	
ESEFQAALS RKVAKL	<u>1951</u>	15	Human	MAGE6	102	
IGHLYIFATCLGLSYD GL	<u>1952</u>	18	Human	MAGE6	172	
VGNWQYFFPVIFSKAS	<u>1953</u>	31	Human	MAGE6	140	
DSLQLVFGIELMEVD	<u>1954</u>	15	Human	MART1	102	
PAYEKLSAEQSPPPY	<u>1955</u>	23	Human	MART1	51	
RNGYRALMDKSLHV GTQCALTRR	<u>1956</u>	14	Human	MBP		A
FFKNIVTFFKNIVT	<u>1957</u>	20	Human	MBP	134	
YKSAHKGFGKGVDAQ GTLSKI	<u>1958</u>	20	Human	MBP	144	
VDAQGTLSKIFKLGG RDSRS	<u>1959</u>	23	Human	MBP	1	
AC-ASQKRPSQRHGS KYL ATAST	<u>1960</u>	15	Human	MBP	85	
ENPVVHFFKNIVTPR						

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
ENPVVAFFKNIVTPR	<u>1961</u>	15	Human	MBP	85	SAAS
ENPVVHAFKNIVTPR	<u>1962</u>	15	Human	MBP	85	SAAS
ENPVVHFFANIVTPR	<u>1963</u>	15	Human	MBP	85	SAAS
ENPVVHFFKNIVTPA	<u>1964</u>	15	Human	MBP	85	SAAS
NPVVHFFKNIVT	<u>1965</u>	12	Human	MBP	86	
HFFKNIVTPRTPPY	<u>1966</u>	14	Human	MBP	90	
NPVVHFFKNIVTPR	<u>1967</u>	14	Human	MBP	86	
LPVPGVLLKEFTVSGN	<u>1968</u>	20	Human	NY-ESO-1	116	
ILTI						
WITQCFLPVFLAQPPS	<u>1969</u>	20	Human	NY-ESO-1	161	
GQRR						
DHRQLQLSISSCLQQL	<u>1970</u>	20	Human	NY-ESO-1	141	
SLLM						
YLAMPFATPMEAELA	<u>1971</u>	20	Human	NY-ESO-1	91	
RRSLA						
AAPLLLARAASLSLG	<u>1972</u>	15	Human	PAP	3	
APLLLARAASLSLGF	<u>1973</u>	15	Human	PAP	4	
PLLLARAASLSLGFL	<u>1974</u>	15	Human	PAP	5	
SLSLGFLFLFFWLD	<u>1975</u>	15	Human	PAP	13	
LLFFWLDRSVLAKEL	<u>1976</u>	15	Human	PAP	21	
DRSVLAKELKFVTLV	<u>1977</u>	15	Human	PAP	27	
AKELKFVTLVFRHGD	<u>1978</u>	15	Human	PAP	32	
RSPIDTFPTDPIKES	<u>1979</u>	15	Human	PAP	47	
FGQLTQLGMEQHYEL	<u>1980</u>	15	Human	PAP	67	
DRTLMSAMTNLAALF	<u>1981</u>	15	Human	PAP	110	
MSAMTNLAALFPPEG	<u>1982</u>	15	Human	PAP	114	
MTNLAALFPPEGVSI	<u>1983</u>	15	Human	PAP	117	
PEGVSIWNPILLWQP	<u>1984</u>	15	Human	PAP	126	
GVSIWNPILLWQPIP	<u>1985</u>	15	Human	PAP	128	
WNPILLWQPIPVHTV	<u>1986</u>	15	Human	PAP	132	
NPILLWQPIPVHTVP	<u>1987</u>	15	Human	PAP	133	
PILLWQPIPVHTVPL	<u>1988</u>	15	Human	PAP	134	
ILLWQPIPVHTVPLS	<u>1989</u>	15	Human	PAP	135	
WQPIPVHTVPLSEDQ	<u>1990</u>	15	Human	PAP	138	
LSGLHGQDLFGIWSK	<u>1991</u>	15	Human	PAP	194	
YDPLYCESVHNFTLP	<u>1992</u>	15	Human	PAP	210	
LPSWATEDTMTKLRE	<u>1993</u>	15	Human	PAP	223	
LRELSELSLLSLYGI	<u>1994</u>	15	Human	PAP	235	
LSELSLLSLYGIHKQ	<u>1995</u>	15	Human	PAP	238	
LSLLSLYGIHKQKEK	<u>1996</u>	15	Human	PAP	241	
KSRLQGGVLVNEILN	<u>1997</u>	15	Human	PAP	255	
GGVLVNEILNHMKRA	<u>1998</u>	15	Human	PAP	260	
IPSYKKLIMYSAHDT	<u>1999</u>	15	Human	PAP	277	
YKKLIMYSAHDTTVS	<u>2000</u>	15	Human	PAP	280	
LIMYSAHDTTVSGLQ	<u>2001</u>	15	Human	PAP	283	
DTTVSGLQMALDVYN	<u>2002</u>	15	Human	PAP	290	
ALDVYNGLLPPYASC	<u>2003</u>	15	Human	PAP	299	
LDVYNGLLPPYASCH	<u>2004</u>	15	Human	PAP	300	

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Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
YNGLLPPYASCHLTE	<u>2005</u>	15	Human	PAP	303	
FAELVGPVIPQDWST	<u>2006</u>	15	Human	PAP	356	
TVPLSEDQLLYLPFR	<u>2007</u>	15	Human	PAP	145	
LTELYFEKGEYFVEM	<u>2008</u>	15	Human	PAP	315	
GPVIPQDWSTECMTT	<u>2009</u>	15	Human	PAP	361	
QAHS�ERVCHCLGKW		21	Human	PLP	130	
LGHDPK	<u>2010</u>					
WTTCQSIAPFSKTSASI		20	Human	PLP	181	
GSL	<u>2011</u>					
QKGRGYRGQHQHS		20	Human	PLP	121	
LERVCH	<u>2012</u>					
AATYNFAVLKLMGR		18	Human	PLP	260	
GTKF	<u>2013</u>					
VATGLCFFGVALFCG		20	Human	PLP	21	
CGHEA	<u>2014</u>					
FLYGALLAEGFYTT		20	Human	PLP	81	
GAVRQ	<u>2015</u>					
SAVPVYIYFNTWTTC		20	Human	PLP	171	
QSIAP	<u>2016</u>					
TLSVTWIGAAPLILS	<u>2017</u>	15	Human	PSA	5	
SVTWIGAAPLILSRI	<u>2018</u>	15	Human	PSA	7	
VTWIGAAPLILSRIV	<u>2019</u>	15	Human	PSA	8	
SQPWQVLVASRGRAV	<u>2020</u>	15	Human	PSA	31	
GRAVCGGVLVHPQW		15	Human	PSA	42	
V	<u>2021</u>					
GVLVHPQWVLTAAH		15	Human	PSA	48	
C	<u>2022</u>					
HPQWVLTAAHCIRNK	<u>2023</u>	15	Human	PSA	52	
QWVLTAAHCIRNKSV	<u>2024</u>	15	Human	PSA	54	
AHCIRNKSVILLGRH	<u>2025</u>	15	Human	PSA	60	
SVILLGRHSLFHPED	<u>2026</u>	15	Human	PSA	67	
VILLGRHSLFHPEDT	<u>2027</u>	15	Human	PSA	68	
GQVFQVSHSFPHPLY	<u>2028</u>	15	Human	PSA	83	
VFQVSHSFPHPLYDM	<u>2029</u>	15	Human	PSA	85	
PHPLYDMSLLKNRFL	<u>2030</u>	15	Human	PSA	93	
SHDMLLLRLSEPAEL	<u>2031</u>	15	Human	PSA	114	
HDLMLLLRLSEPAELT	<u>2032</u>	15	Human	PSA	115	
TDAVKVMDLPTQEPA	<u>2033</u>	15	Human	PSA	129	
LHVISNDVCAQVHPQ	<u>2034</u>	15	Human	PSA	172	
CAQVHPQKVTKFMLC	<u>2035</u>	15	Human	PSA	180	
GGPLVCNGVLQGITS	<u>2036</u>	15	Human	PSA	210	
GPLVCNGVLQGITSW	<u>2037</u>	15	Human	PSA	211	
NGVLQGITSWGSEPC	<u>2038</u>	15	Human	PSA	216	
RPSLYTKVVHYRKWI	<u>2039</u>	15	Human	PSA	235	
HSLFHPEDTGQVFQV	<u>2040</u>	15	Human	PSA	74	
PRWLCAGALVLAGGF	<u>2041</u>	15	Human	PSM	18	
LGFLFGWFIKSSNEA	<u>2042</u>	15	Human	PSM	35	
LDELKAENIKKFLYN	<u>2043</u>	15	Human	PSM	62	
IKKFLYNFTQIPH LA	<u>2044</u>	15	Human	PSM	70	
KFLYNFTQIPHLAGT	<u>2045</u>	15	Human	PSM	72	
WKEFGLDSVELAHYD	<u>2046</u>	15	Human	PSM	100	

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Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
LAHYDVLLSYPNKTH	<u>2047</u>	15	Human	PSM	110	
GNEIFNTSLFEPPPP	<u>2048</u>	15	Human	PSM	135	
GKVFRGNKVKNACL	<u>2049</u>	15	Human	PSM	206	
A	<u>2050</u>	15	Human	PSM	211	
GNKVKNACLAKG	<u>2051</u>	15	Human	PSM	276	
V	<u>2052</u>	15	Human	PSM	284	
EYAYRRGIAEAVGLP	<u>2053</u>	15	Human	PSM	286	
AEAVGLPSIPVHPIG	<u>2054</u>	15	Human	PSM	297	
AVGLPSIPVHPIGYY	<u>2055</u>	15	Human	PSM	334	
IGYYDAQKLEKMG	<u>2056</u>	15	Human	PSM	353	
TGNFSTQKVKMHIHS	<u>2057</u>	15	Human	PSM	444	
TRIYNVIGTLRGAVE	<u>2058</u>	15	Human	PSM	446	
ERGVAYINADSSIEG	<u>2059</u>	15	Human	PSM	453	
GVAYINADSSIEGNY	<u>2060</u>	15	Human	PSM	459	
DSSIEGNYTLRVDCT	<u>2061</u>	15	Human	PSM	466	
NYTLRVDCTPLMYSL	<u>2062</u>	15	Human	PSM	520	
CTPLMYSLVHNLTK	<u>2063</u>	15	Human	PSM	522	
E	<u>2064</u>	15	Human	PSM	543	
DFEVFFQRLGIASGR	<u>2065</u>	15	Human	PSM	566	
EVFFQRLGIASGRAR	<u>2066</u>	15	Human	PSM	567	
TNKFSGYPLYHSVYE	<u>2067</u>	15	Human	PSM	569	
YDPMFKYHLTVAQVR	<u>2068</u>	15	Human	PSM	571	
DPMFKYHLTVAQVRG	<u>2069</u>	15	Human	PSM	576	
MFKYHLTVAQVRGG	<u>2070</u>	15	Human	PSM	580	
M	<u>2071</u>	15	Human	PSM	582	
KYHLTVAQVRGGMV	<u>2072</u>	15	Human	PSM	584	
F	<u>2073</u>	15	Human	PSM	608	
VAQVRGGMVFELANS	<u>2074</u>	15	Human	PSM	611	
RGGMVFEANSIVLP	<u>2075</u>	15	Human	PSM	619	
GMVFELANSIVLPFD	<u>2076</u>	15	Human	PSM	624	
VFELANSIVLPFDCR	<u>2077</u>	15	Human	PSM	660	
ADKIYSISMKHPQEM	<u>2078</u>	15	Human	PSM	661	
IYSISMKHPQEMKTY	<u>2079</u>	15	Human	PSM	688	
PQEMKTYSVSFDSL	<u>2080</u>	15	Human	PSM	730	
TYSVSFDSLFSVKN	<u>2081</u>	15	Human	PSM	731	
VLRMMNDQLMFLER	<u>2082</u>	15	Human	PSM	734	
A	<u>2083</u>	15	Human	PSM	127	
LRMMNDQLMFLERA	<u>2084</u>	15	Human	PSM	128	
F	<u>2085</u>	15	Human	PSM	183	
RHVIYAPSSHNYAG	<u>2086</u>	15	Human	PSM	185	
RQIYVAAFTVQAAAE	<u>2087</u>	15	Human	PSM	224	
QIYVAAFTVQAAAE	<u>2088</u>	15	Human	PSM	391	
QIYVAAFTVQAAAE	<u>2089</u>	15	Human	PSM	438	
VAAFTVQAAAE						
TLSE						
YISIINEDGNEIFNT						
ISIINEDGNEIFNTS						
EDFFKLERDMKINCS						
FFKLERDMKINCSGK						
GVILYSDPADYFAPG						
GAAVVHEIVRSFGTL						
NSRLLQERGVAYINA						

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Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
VAYINADSSIEGNYT	<u>2090</u>	15	Human	PSM	447	
DQLMFLERAFIDPLG	<u>2091</u>	15	Human	PSM	666	
KSNFLNCYVSGFHPSD	<u>2092</u>	16	Human B2- μglobulin		19	
AC- NPDAENWNSQFEILE DAA	<u>2093</u>	18	IEd	MHC derived	Unknown	
EYLILSARDVLAVVS	<u>2094</u>	15	M. leprae		85	
YKTIA YDEEARR	<u>2095</u>	12	MT		3	
GEALSTLVVNKIRGT	<u>2096</u>	15	Mycobacteria	HSP60	254	
PYILLVSSKVSTVKD	<u>2097</u>	15	Mycobacteria	HSP60	216	
EAVLEDPYILLVSSK	<u>2098</u>	15	Mycobacteria	HSP60	210	
IAGLFLTTEAVVADK	<u>2099</u>	15	Mycobacteria	HSP60	507	
ALSTLVVNKIRGTFK	<u>2100</u>	15	Mycobacteria	HSP60	256	
MKHILYISFYFILVN	<u>2101</u>	15	Pf	LSA1	1	
KSLSTNLPYGRTNL	<u>2102</u>		Pf	SSP2	116	
HFFLLYILFLVKM	<u>2103</u>	15	Pf		13	
LFLLYILFLVKMNAL	<u>2104</u>	15	Pf		16	
ILFLVKMNALRRLPV	<u>2105</u>	15	Pf		21	
MNALRRLPVICSFLV	<u>2106</u>	15	Pf		27	
SAFLESQSMNKIGDD	<u>2107</u>	15	Pf		79	
LKELIKVGLPSFENL	<u>2108</u>	15	Pf		132	
FENLVAENVKPPKVD	<u>2109</u>	15	Pf		143	
PATYGIIVPVLTSLF	<u>2110</u>	15	Pf		158	
YGIIVPVLTSLFNKV	<u>2111</u>	15	Pf		161	
LLKIWKNYMKIMNHL	<u>2112</u>	15	Pf		28	
MTLYQIQVMKRNQK	<u>2113</u>	15	Pf		43	
Q	<u>2113</u>					
QKQVQMMIMIKFMG	<u>2114</u>	15	Pf		57	
V	<u>2114</u>					
MIMIKFMGVIYIMII	<u>2115</u>	15	Pf		63	
GVIYIMIISKMMRK	<u>2116</u>	15	Pf		70	
LYYLFNQHIKKELYH	<u>2117</u>	15	Pf		285	
HFNMLKNKMQSSFFM	<u>2118</u>	15	Pf		299	
LDIYQKLYIKQEEQK	<u>2119</u>	15	Pf		353	
QKKYIYNLIMNTQNK	<u>2120</u>	15	Pf		366	
YEALIKLLPFSKRIR	<u>2121</u>	15	Pf		381	
ENEYATGAVRPFQAA	<u>2122</u>	15	Pf		2	
NYELSKAVIFTPIY	<u>2123</u>	15	Pf		27	
QKILIKIPVTKNIIT	<u>2124</u>	15	Pf		108	
KCLVISQVSNSDSYK	<u>2125</u>	15	Pf		156	
SKIMKLPKLPISNGK	<u>2126</u>	15	Pf		202	
FIHFFTWTGTMFVPKY	<u>2127</u>	15	Pf		220	
LCNFKKNIIALLIIP	<u>2128</u>	15	Pf		242	
KKNIIALLIIPPKIH	<u>2129</u>	15	Pf		246	
ALLIIPPKIHISIEL	<u>2130</u>	15	Pf		251	
SMEYKKDFLITARKP	<u>2131</u>	15	Pf		274	
KSKFNILSSPLFNNF	<u>2132</u>	15	Pf		7	

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
FKKLKNHVLFLQMM		15	Pf		173	
N	<u>2133</u>					
KNHVLFLQMMNVNL		15	Pf		177	
Q	<u>2134</u>					
VLFLQMMNVNLQKQ		15	Pf		180	
L	<u>2135</u>					
NVNLQKQLLTNHLIN	<u>2136</u>	15	Pf		187	
QKQLLTNHLINTPKI	<u>2137</u>	15	Pf		191	
NHLINTPKIMPHHII	<u>2138</u>	15	Pf		197	
YILLKKILSSRFNQM	<u>2139</u>	15	Pf		239	
FNQMIFVSSIFISFY	<u>2140</u>	15	Pf		250	
KVSCKGSGYTFTAYQ		17	Rheumatiod	Variable		
MH	<u>2141</u>		vector	region		
IAKVPPGPNITAEYGD		20	Rye grass	Lolp1	1	
KWLD	<u>2142</u>					
TAEYGDKWLDKST		20	Rye grass	Lolp1	11	
WYGKPT	<u>2143</u>					
AKSTWYGKPTGAGPK		20	Rye grass	Lolp1	21	
DNGGA	<u>2144</u>					
GAGPKDNGGACGYK		20	Rye grass	Lolp1	31	
DVDKAP	<u>2145</u>					
FNGMTGCGNTPIFKD		20	Rye grass	Lolp1	51	
GRGCG	<u>2146</u>					
PIFKDGRGCGSCFEIK		20	Rye grass	Lolp1	61	
CTKP	<u>2147</u>					
SCFEIKCTKPESCSGE		20	Rye grass	Lolp1		
AVTV	<u>2148</u>					
AFGSMAKKGEEQNVNR		20	Rye grass	Lolp1	111	
SAGEL	<u>2149</u>					
TPDKLTGPFTVRYTTE		20	Rye grass	Lolp1	201	
GGTK	<u>2150</u>					
VRYTTEGGTKSEVED		20	Rye grass	Lolp1	211	
VIPEG	<u>2151</u>					
TCVLGKLSQELHKLQ	<u>2152</u>	15	Salmon	Calcitonin	6	
KLSQELHKLQTYPR	<u>2153</u>	15	Salmon	Calcitonin	11	
LHKLQTYPRNTGSG	<u>2154</u>	15	Salmon	Calcitonin	16	
KLQTYPRNTGSGTP	<u>2155</u>	15	Salmon	Calcitonin	18	
CCVLGKLSQELHKLQ	<u>2156</u>	15	Salmon	Calcitonin	7	A
CSNLSTCVLGKLSQE	<u>2157</u>	15	Salmon	Calcitonin	1	A
TSNLSTTVLGKLSQE	<u>2158</u>	15	Salmon	Calcitonin	1	A
TTVLGKLSQELHKLQ	<u>2159</u>	15	Salmon	Calcitonin	6	A
DIAAKYKELGY	<u>2160</u>	11	Sperm whale	Myoglobin	141	
ALVRQGLAKVA	<u>2161</u>	11	Staph.	Nase	102	
PATLIKAIDGDTVKLM		20	Staph.	Nase	11	
YKGQ	<u>2162</u>					
TPETKHPKKGVEKYG		20	Staph.	Nase	41	
PEASA	<u>2163</u>					
VEKYGPEASAFTKKM		20	Staph.	Nase	51	
VENAK	<u>2164</u>					
FTKKMVENAKKIEVE		20	Staph.	Nase	61	
FDKGQ	<u>2165</u>					
YIYADGKMVNEALVR		20	Staph.	Nase	91	
QGLAK	<u>2166</u>					
HEQHRLRKSEAQAKKE		20	Staph.	Nase	121	
KLNIW	<u>2167</u>					
QAKKEKLNIWSEDNA		19	Staph.	Nase	131	
DSGQ	<u>2168</u>					

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
YFNNFTVSFWLRVPK	<u>2169</u>	15	TetTox		947	
FSYFPSI	<u>2170</u>	7	TetTox		593	A
YSFFPSI	<u>2171</u>	7	TetTox		593	A
YSYFPSIR	<u>2172</u>	8	TetTox		593	A
DPNANPNVDPNANPN VNANPNANPNANP(X 4)	<u>2173</u>	117	Unknown	(MAP)=(T1B)4		
QKWAAVVVPS	<u>2174</u>	10	Unknown	ClassI A2	242	
TWQLNGEELIQDMEL VETRPAG	<u>2175</u>	22	Unknown	ClassI Kb 216-237	216	
PEFLEQRRAAVDTYC	<u>2176</u>	15	Unknown	IEBs2		
STORKUSP33			Unknown	RAGE		
DYSYLQSDSPDSFQD	<u>2178</u>	15	Unknown	Tyrosinase	448	
DFSYLQSDSPDSFQD	<u>2179</u>	15	Unknown	Tyrosinase	448	SAAS
QNILFSNAPLGPQFP	<u>2180</u>	15	Unknown	Tyrosinase	56	SAAS
QNILLSNAPLVPQFP	<u>2181</u>	15	Unknown	Tyrosinase	56	SAAS
DYSYLQSDSPDSFQD	<u>2182</u>	15	Unknown	Tyrosinase	448	
KYVKQNTLKLAT	<u>2183</u>	11	unknown			
P(X)KQNTLKLAT	<u>2184</u>	13	unknown			A
EEDIEIPIQEEY	<u>2185</u>	14		CD20	249	A
HQAISPRTLNSPAIF	<u>2186</u>	15				
YTDVFSLDPTFTIETT	<u>2187</u>	16				
YAGIRRDGLLLRLVD	<u>2188</u>	15				A
LEFYRKSVWSKLQSI	<u>2189</u>	15				
RPIVNMDYVVGARTF		20				
RREKR	<u>2190</u>					
RPGLLGASVLGLDDI	<u>2191</u>	15				
LYFVKVDVTGAYDTI	<u>2192</u>	15				
FAGIRRDGLLLRLVD	<u>2193</u>	15				
AKTFLRTLVRGVPEY	<u>2194</u>	15				
YGAVVNLRKTVVNFP	<u>2195</u>	15				
GTAFVQMPAHGLFPW	<u>2196</u>	15				
WAGLLDTRTLEVQS	<u>2197</u>	15				
RTSIRASLTFNRGFK	<u>2198</u>	15				
RVIKNSIRLTL	<u>2199</u>	11				
PVIKNSIKLRL	<u>2200</u>	11				
ATSTKKLHKPATLIK		21				
AIDG	<u>2201</u>					

TABLE 26

[illegible]

HLA-DR SUPERTYPE									
Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
(43)AAFFGIFKIGKF A	<u>1578</u>	50000		381	500000				
(43)AADFGIFIDFIIA A	<u>1579</u>	50000		235	500000				
(43)AAIGGIFIFKKD A	<u>1580</u>	50000		800	500000				
(43)AAFIGFGKIKFI A	<u>1581</u>	50000		1000	500000				
(43)AAKIGFGIKIGF A	<u>1582</u>	50000		1000	500000				
(43)AAFKIGKFGIFF A	<u>1583</u>	50000		276	500000				
AAAKAAAAAAAAA F	<u>1584</u>	>1666.67		>347.83	12500				
AAAKAAAAAAAF A	<u>1585</u>	50000		727	500000				
AAAKAAAAAFA A	<u>1586</u>	50000		235	25000				
AAKAAAAFAAA A	<u>1587</u>	50000		533	500000				
FAAAAAAAAAA A	<u>1588</u>	1667		200	8333				
AAAAAAAAAAAA N	<u>1589</u>	50000		500	500000				
AAAAAAAAAAAAAN A	<u>1590</u>	50000		1000	500000				
AAANAAAAAAAAA A	<u>1591</u>	50000		615	500000				
AAAAAAAAAAAAA S	<u>1592</u>	50000		533	500000				
AAAAASAAAAA A	<u>1593</u>	50000		235	500000				
ASAAAAAAAAA A	<u>1594</u>	50000		364	500000				
AFAAAKTAA A	<u>1595</u>	50000		571	500000				
YARFLALTTLRAR A	<u>1596</u>	0.98		0.28	3.4				
YAR(15A)SQTTLKA KT	<u>1597</u>	2.4		0.78	5.2		1786		
YAR(15A)RQTTLKA AA	<u>1598</u>	1.6		0.35	3.8		8333		
(15A)RQTTLKAAA A	<u>1599</u>	4.2		0.31	4.3		250000		
(16A)RQTTLKAAA A	<u>1600</u>	455		1.3	37		250000		
(46)AAKTAAFA A	<u>1601</u>	5000		571	1852				
(39)AAAAATKAAA A	<u>1602</u>	3333		727	500000				
(52)AAAAATKAAAA A	<u>1603</u>	2000		242	2632				
(55)AAAAATKAAAA A	<u>1604</u>	2500		667	5556				
A(14)AAAKTAAA AA	<u>1605</u>	39		0.45	54		96		
AA(14)A(35)ATKAA AA	<u>1606</u>	50000		>500	500000				
AA(14)AA(36)TKAA AA	<u>1607</u>	50000		667	25000				
AFAAAKTAA(72) A	<u>1608</u>	5000		533	500000				
(49)AAAKT(64)AAA A	<u>1609</u>	50000		667	500000				
(49)AAAKTA(64)AA A	<u>1610</u>	50000		533	500000				
HQAISPRTLNGPGP GSPAIF	<u>1611</u>	1555	728464	12089	2056	3107	5081		
YAAFAAAKTAAAF A	<u>1612</u>	1.9		0.82	7.0				
TEGRCLHYTVDKS KPK	<u>1613</u>	1667		200	500000		>250000		
AWVAWRNRCK A	<u>1614</u>	50000		667	500000		>12500		
IVSDGNGMNAWV AWRNRC	<u>1615</u>	1250	18371	1000	8333		>8333.33		

HLA-DR SUPERTYPE									
Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
PHHTALRQAILSW		1250		166	1773		14434		
GELMTLA	<u>1616</u>								
WMYYHGQRHSDE		50000	>900000	727	500000		>250000		
HHH	<u>1617</u>								
YIVMSDWTGGA	<u>1618</u>	50000	13416	222	500000		12500		
AHAHAHAHAHA		263		80000	500000		>250000		
AHAA	<u>1619</u>								
MDIDPYKEFGATV		1563		170			6609		
ELLSFLPSDFFP	<u>1620</u>								
GMLPVCPLIPGSST		1250	>900000	400	1220		250000		
TSTGP	<u>1621</u>								
LGFFPDHQLDPAFR		1667	12027	333	2941		250000		
ANT	<u>1622</u>								
GYKVLVLNPSV	<u>1623</u>	16	72407	27	2116	145	1516	115	8789
LMAFTAAVTS	<u>1624</u>	2511	>73952.34	321	20577	627	240	>40562.91	160
TFALWRVSABEY	<u>1625</u>	>5279.83	88348	342	569	72	927	1433	517
ALWRVSABEY	<u>1626</u>	>6337.14	>76595.74	6543	6669	>35315.99	7954	4099	698
EEYVEIRQVGDFH	<u>1627</u>	>1957.71	74884	>5365.53	11627	26	11323	13890	11154
VGGVYLLPRRGPR		177	236639	22323	12756	2764	351		
LGV	<u>1628</u>								
VGGAYLLPRRGPR		131	308534	26164	125056	>12230.45	703		
LGV	<u>1629</u>								
VGGVALLPRRGPR		849	326288	48233	23669	>12230.45	61558		
LGV	<u>1630</u>								
VGGVYALPRRGPR		134	348950	25750	30504	>12230.45	749		
LGV	<u>1631</u>								
VGGVYLAPRRGPR		746	202660	33672	>116550.12	>12230.45	878		
LGV	<u>1632</u>								
VGGVYLLARRGPR		60	23276	485	4396	2199	595		
LGV	<u>1633</u>								
VGGVYLLPARGPR		12	68070	3644	3213	4579	49		
LGV	<u>1634</u>								
VGGVYLLRRAGPR		202	39751	12252	32330	6432	433		
LGV	<u>1635</u>								
GAPLGGAARALAH		690	3145	10408	19762	>13044.97	10773		
GV	<u>1636</u>								
GAALGGAARALAH		1081	26944	21362	60600	>13044.97	29786		
GV	<u>1637</u>								
GAPLAGAARALAH		588	2983	39885	19692	>13044.97	8178		
GV	<u>1638</u>								
GAPLGAAARALAH		226	17703	10255	52041	>13044.97	6490		
GV	<u>1639</u>								
GAPLGLARALAH		537	351525	13941	6564	>13044.97	66		
GV	<u>1640</u>								
GAPLGALRALAH		68	>486486.49	14977	977	1271	1418		
GV	<u>1641</u>								
GAPLGGAALALAH		147	82088	5472	1272	>3365.21	31907		
GV	<u>1642</u>								
GAPLGGAARLLAH		398	22959	14984	21017	>3365.21	57549		
GV	<u>1643</u>								
GAPLGGAARAAAHA		797	377964	25279	>110132.16	>3365.21	31308		
GV	<u>1644</u>								
GAPLGGAARALAA		541	23298	11270	16747	>3365.21	7419		
GV	<u>1645</u>								
FPDWQNYTPGPGT		13766	>223880.6	23394	>109170.31	>10101.01	59625	592	3013
RF	<u>1646</u>								
RFPLTFGWCFKLV		5913	406579	316	21384	121	4100	748	1848
V	<u>1647</u>								
RQDILDWVYHTQ		2390	98327	1202	1624	1136	1628	5039	1665
GY	<u>1648</u>								
RQEILDWVYHTQ		1050	10530	5928	1414	3362	3052	2730	3679
GF	<u>1649</u>								
LSHFLKEKGGLEGL		537	>340909.09	2442	86814	2114	13676	1561	23191
I	<u>1650</u>								
LSFFLKEKGGLDGL		172	>340909.09	1275	>109170.31	983	19957	1127	3501
I	<u>1651</u>								
LEPNWHPGSQPKT		>33557.05	>328467.15	>33333.3	>96525.1	>8232.24	>72254.34	69223	34468
ACT	<u>1652</u>			3					

HLA-DR SUPERTYPE									
Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
QVCFITKGLGISYG		114	166744	1529	1391	295	91	41	296
R	<u>1653</u>								
QLCFLKKGGLGISYG		185	158381	4436	1613	443	3634	40	200
R	<u>1654</u>								
PPEESFRFGEEKTTP		>2500	>900000	267	500000		>12500		
S	<u>1655</u>								
CIVYRDGNPYAVC		8464		147	1084	3473	>17182.13		31865
DK	<u>1656</u>								
HYCYSLYGTTLEQ		546		1127	9713	76	9858		12359
QY	<u>1657</u>								
CYSLYGTTLEQQY		1086		1317	2836	71	>9964.13		25989
NK	<u>1658</u>								
NTSLQDIEITCVYC		>12106.54		10930	6143	4584	>17182.13		30884
K	<u>1659</u>								
VFEFAFKDLFVVYR		6716		1059	2156	120	11583		16797
D	<u>1660</u>								
EFAFKDLFVVYRDS		8944		2220	11721	33	3688		1882
I	<u>1661</u>								
DLFVVYRDSIPHAA		1186		82	218	3591	5213		2374
C	<u>1662</u>								
FVVYRDSIPHAACH		587	200	10	87	704	5085		2122
K	<u>1663</u>								
NTGLYNLLIRCLRC		127	13429	686	358	258	6743		4759
Q	<u>1664</u>								
IRCLRCQKPLNPAE		7240		6334	8464	1229	16787		32024
K	<u>1665</u>								
PRKLHELSSALEIPY		156	16146	5276	694	80	103		213
EIPYDELRLNVCYC		3299		15532	11292	7321	>35612.54		>39432.18
K	<u>1667</u>								
TEVLDFAFDTLTIV		2073	1542	185	1083	871	1432		349
Y	<u>1668</u>								
VLDFAFTDLTIVYR		354	30	313	6061	721	230		252
D	<u>1669</u>								
DFAFTDLTIVYRDD		463	23	80	3373	40	725		1443
T	<u>1670</u>								
TIVYRDDTPHGVCT		3798		22	1269	>9753.59	>35612.54		>39144.05
K	<u>1671</u>								
WYRYSVYGTITLEK		163	26561	249	3448	8.5	107		284
LT	<u>1672</u>								
ETTIHNIELQCVEC		3623		1996	3327	6561	>35612.54		>39432.18
K	<u>1673</u>								
SEVYDFAFADLTIV		31	2996	260	2180	101	1850		174
VY	<u>1674</u>								
VYDFAFADLTVVY		173		119	5281	133	7012		155
RE	<u>1675</u>								
DFAFADLTVVYRE		3293		141	4948	60	1728		322
GN	<u>1676</u>								
TVVYREGNPFGICK		168		121	1833	>13089.91	10064		2407
L	<u>1677</u>								
GNPFGICKLCLRFL		189		1227	2073	377	13916		45631
S	<u>1678</u>								
NYSVYGNLTLEQTV		14059		1933	91506	822	>14602.8		47481
KK	<u>1679</u>								
KKPLNEILIRCIICQ		1363		315	1070	347	7972		13328
NEILIRCIICQRPLC		7945		11739	23082	7704	16901		26483
IRCIICQRPLCPQEK		7549		5960	23092	2973	>14602.8		40269
CIVYRDCIAYAACH		1166		928	8560	3973	>14602.8		10186
K	<u>1683</u>								
NTELYNLLIRCLRC		1108		1366	1293	873	>14602.8		12528
Q	<u>1684</u>								
IRCLRCQKPLNPAE		7012		6668	9890	8982	>14602.8		>32271.94
K	<u>1685</u>								
REVYKFLFTDLRIV		8.7	23	112	738	52	54		204
Y	<u>1686</u>								
RIVYRDNNPYGVCI		524	325	20	432	2307	8307		24147
M	<u>1687</u>								
NNPYGVCIMCLRFL		1075		1378	2522	454	12020		30895
S	<u>1688</u>								

HLA-DR SUPERTYPE									
Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
EERVKKPLSEITIRC	<u>1689</u>	1286		11896	9772	1470	9454		19968
IRCIICQTPLCPEEK	<u>1690</u>	10847		12270	3812	1407	25186		28062
EIPLIDLRLSCVYCK	<u>1691</u>	7610		1876	5012	336	10468		1961
SCVYCKKELTRAE		6466		2411	7510	465	8446		2010
VY	<u>1692</u>								
VCLLFYSKVRKYR		960	276	286	987	73	258		1798
YY	<u>1693</u>								
YYDYSVYGATLESI		1008		186	9855	230	744		1403
T	<u>1694</u>								
IRCYRCQSPLTPEE		10947		13358	83166	10327	13356		>36023.05
K	<u>1695</u>								
VYDFVFADLRIVYR		98	2.2	475	5856	717	5962		198
D	<u>1696</u>								
DFVFADLRIVYRDG		6699		867	7197	133	9847		1962
N	<u>1697</u>								
RIVYRDGNPFAVC		116	144	19	209	1812	6638		4962
KV	<u>1698</u>								
GNPFAVCVKVCLRL		134	3805	322	522	56	1034		29300
LS	<u>1699</u>								
KKCLNEILIRCIICQ	<u>1700</u>	9357		424	1229	365	16288		3997
NEILIRCIICQRPLC	<u>1701</u>	10992		14069	9339	4621	18947		22062
RTAMFQDPQERPR		9372	154	28192	39014	7977	32947		>25346.4
KL	<u>1702</u>								
LFVVYRDSIPHAAC		131	62	3.0	24	690	1998		2855
H	<u>1703</u>								
LTIVYRDDTPHGVCT		>15384.62	187	23	203	>8593.4	>72254.34		>25346.4
T	<u>1704</u>								
LCIVYRDCIAYAAC		996	1855	357	1293	628	40121		10660
H	<u>1705</u>								
YKFLFTDLRIVYRD		109	8.8	292	256	91	1516		1255
N	<u>1706</u>								
YNFACTELKLVR		7522	346	1976	4246	3147	2867		2084
DD	<u>1707</u>								
LKLVYRDDFPYAV		778	237	123	9269	830	28971		18677
CR	<u>1708</u>								
YDFVFADLRIVYRD		1160	13	1914	3264	829	21352		5419
G	<u>1709</u>								
LRIVYRDGNPFAVC		142	181	16	25	557	8985		14207
K	<u>1710</u>								
HEYMLDLQPETTD		1377		222	3997	2291	>18559.76		21277
LY	<u>1711</u>								
TLRLCVQSTHVDIR		1517		11996	8650	169	3257		6368
T	<u>1712</u>								
IRTLEDLLMGTGLGI		16	5211	95	43	61	895		1718
V	<u>1713</u>								
LEDLLMGTGLGIVCP		104		1136	353	1116	261		1994
I	<u>1714</u>								
DLLMGTGLGIVCPIC		966		1324	984	639	963		2614
S	<u>1715</u>								
KATLQDIVLHLEPQ		1204		1987	811	1173	9094		17726
N	<u>1716</u>								
IDGVNHQHLPARR		1060		34272	165545	>16971.86	>18559.76		>39914.85
AE	<u>1717</u>								
LRAFQQLFLNTLSF		1.5	648	7.4	13	8.3	75		174
V	<u>1718</u>								
FQQLFLNTLSFVCP		118	1321	134	1585	222	134		2062
W	<u>1719</u>								
QDYVLDLQPEATD		13441		253	45281	5585	>18559.76		>39914.85
LH	<u>1720</u>								
DIRILQELLMGSFGI		88	3252	166	290	552	1591		282
	<u>1721</u>								
IRILQELLMGSFGIV		67	31840	724	710	1208	1998		271
	<u>1722</u>								
ELLMGSFGIVCPNC		628		1078	8518	1853	4183		949
S	<u>1723</u>								
KEYVLDLYPEPTDL		5949		131	89674	391	>72254.34		>49867.02
Y	<u>1724</u>								
LRTIQQLLMGTVNI		13	23182	108	208	179	513		181
V	<u>1725</u>								

HLA-DR SUPERTYPE									
Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
IQQLMGTVNIVCP		71	93701	107	483	624	444		156
T	<u>1726</u>								
QLLMGTVNIVCPTC		1192		2874	10062	4688	2947		2209
A	<u>1727</u>								
RETLQEIVLHLEPQ		1592		2941	6583	829	25856		19109
N	<u>1728</u>								
LRTLQQLFLSTLSF		8.3	801	18	18	9.0	60		166
V	<u>1729</u>								
LQQLFLSTLSFVCP		121	2045	113	754	94	272		152
W	<u>1730</u>								
KDYILDLPETTDL		6409		1022	30309	2771	>72254.34		>49867.02
H	<u>1731</u>								
LRTLQQMLLGTLQ		80	>3750000	437	644	79	6909		5077
VV	<u>1732</u>								
LQQMLLGTLQVVC		168		1496	631	1068	929		1692
PG	<u>1733</u>								
QMLLGTLQVVCPG		957		2773	425	3074	3722		2082
CA	<u>1734</u>								
VPTLQDVVLELTPQ		16056		214	4764	5409	>35360.68		>30612.24
T	<u>1735</u>								
LQDVVLELTPQTEI		1487		101	1094	417	5673		2180
D	<u>1736</u>								
QDVVLELTPQTEID		1269		83	1537	53	2716		1684
L	<u>1737</u>								
CKFVVQLDIQSTKE		1251		196	1642	374	4547		19282
D	<u>1738</u>								
VVQLDIQSTKEDLR		1060		11122	8625	46	3762		13906
V	<u>1739</u>								
DLRVVQQLMGAL		8.4	25971	325	89	84	508		1845
TV	<u>1740</u>								
LRVVQQLMGALT		5.7	21650	115	28	85	82		204
VT	<u>1741</u>								
VQQLMGALTVTC		10	34257	239	614	116	71		180
PL	<u>1742</u>								
QQLMGALTVTCP		75		1142	1286	201	743		1170
LC	<u>1743</u>								
QLLMGALTVTCPL		54	>3750000	595	870	1019	389		303
CA	<u>1744</u>								
REYILDHPEPTDL		154		132	9957	354	7257		29316
F	<u>1745</u>								
TCCYTCGTTVRLCI		1230	19884	719	2269	132	63		1374
N	<u>1746</u>								
VRTLQQLMGCTI		36	32360	322	39	114	1820		496
V	<u>1747</u>								
LQQLMGCTIVCP		197		1147	483	522	2098		1638
S	<u>1748</u>								
MLDLQPETTDLYC		10076	720	1913	12241	4249	>72254.34		>32230.34
YE	<u>1749</u>								
VLDLYPEPTDLYCY		11201	121	203	2193	212	>72254.34		>32230.34
E	<u>1750</u>								
LREYILDHPEPTD		134	891	23	9235	968	21989		16462
L	<u>1751</u>								
HIEFTPTRTDTYAC		50000	30000	667	10000		>12500		
RV	<u>1752</u>								
LWWVNNEPLVSP			315						
RL	<u>1753</u>								
YEEYVRFSDVGE		50000		400	500000		250000		
EEYVRFSDVGE	<u>1754</u>								
EEYVRFSDVGE	<u>1755</u>	50000		216	500000		250000		
APPRICDSRVLER		1374	6.3	9735	5794	7141	8937	11214	9348
Y	<u>1756</u>								
ICDSRVLERYLLEA		2758	236	1984	10984	11016	57605	808	>78947.37
K	<u>1757</u>								
VLERYLLEAKEAE		933	59010	2598	12139	5019	13067	3150	6382
NI	<u>1758</u>								
EHCSLNENITVPDT		9837	27481	2294	28297	1205	32375	6191	>78947.37
K	<u>1759</u>								
NENITVPDTKVNFY		>24154.59	4.8	>21390.3	7612	>18572.83	42846	1850	>78947.37
A	<u>1760</u>			7					
VPDTKVNFYAWKR		2764	259	1742	4131	1328	38622	422	>78947.37
ME	<u>1761</u>								

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Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
VNFYAWKRMEVG		193	2871	10	291	15	40163	35	1238
QQA	<u>1762</u>								
WKRMEVGQQAWE		62	514	24	2591	94	46062	139	14696
VWQ	<u>1763</u>								
VGQQAWEVWQGL		161	>174081.24	10294	6283	923	4230	>40511.09	>78947.37
ALL	<u>1764</u>								
VEVWQGLALLSEA		86	13293	1310	1357	79	6863	13411	8151
VL	<u>1765</u>								
GLALLSEAVLRGQ		83	816	11	21	1435	4606	2000	15148
AL	<u>1766</u>								
SEAVLRGQALLVN		11	70855	2064	4207	17446	1087	>63636.36	>78947.37
SS	<u>1767</u>								
RGQALLVNSSQPW		1118	93874	1697	1168	3434	319	29454	8450
EP	<u>1768</u>								
LVNSSQPWEPLQL		2178	26138	>21505.3	13031	19689	8344	16920	>78947.37
HV	<u>1769</u>			8					
QPWEPLQLHVDKA		11567	4862	1296	6135	1111	24157	>63636.36	34819
VS	<u>1770</u>								
LQLHVDKAVSGLR		192	22	9.7	44	13571	3213	801	>78947.37
SL	<u>1771</u>								
DKAVSGLRSLTTL		13	4331	1014	25	247	615	16375	>78947.37
R	<u>1772</u>								
GLRSLTTLRALGA		8.5	2345	24	9.2	30	509	14	1136
Q	<u>1773</u>								
TTLRALGAQKEAI		19	107164	339	199	103	4281	652	4607
S	<u>1774</u>								
ALGAQKEAISPPDA		194	>204081.63	>21505.3	93062	13015	>71225.07	>60214.56	15337
A	<u>1775</u>			8					
KEAISPPDAASAAP		15531	48560	6590	4389	28755	6661	6391	5735
L	<u>1776</u>								
PPDAASAAPLRTIT		309	14900	566	68	1555	24937	>63636.36	8674
A	<u>1777</u>								
SAAPLRTITADTFR		1166	1262	1185	261	1456	3646	28110	2505
K	<u>1778</u>								
RTITADTFRKLFRV		148	139	1042	928	1957	3448	792	4692
Y	<u>1779</u>								
DTFRKLFRVYSNFL		12	6946	70	104	93	10	39	307
R	<u>1780</u>								
LFRVYSNFLRGKLL		43	6156	643	1816	1275	5.5	28	3508
L	<u>1781</u>								
SNFLRGKLLKLYTGE		143	9583	2883	2375	7182	3783	1433	8099
A	<u>1782</u>								
KLKLYTGEACRTG		122	18435	5964	3505	36294	8082	7683	2860
DR	<u>1783</u>								
APRLITDSRVLER		10144	15	6680	3168	7765	629	26382	8391
Y	<u>1784</u>								
ITDSRVLERYLLEA		1571	6501	1303	1990	13339	7498	967	>78947.37
K	<u>1785</u>								
EHTSLNENITVPDT		43921	33635	12379	2769	1245	37154	>16333.33	>78947.37
K	<u>1786</u>								
KLKLYTGEATRTG		178	118459	15	3230	1426	8234	2008	>78947.37
DR	<u>1787</u>								
PQFRPQQPYYPQ	<u>1788</u>								
PFRPQQPYYPQ	<u>1789</u>								
PQFRPQQPYYP	<u>1790</u>								
PQFRPQQP	<u>1791</u>								
KQFRPQQPYYPQ	<u>1792</u>								
PKFRPQQPYYPQ	<u>1793</u>								
PQPFKPQQPYYPQ	<u>1794</u>								
PQPFRKQQPYYPQ	<u>1795</u>								
PQPFRPQKPYPQ	<u>1796</u>								
PQPFRPQQPKPQ	<u>1797</u>								
PQPFRPQQPYKQ	<u>1798</u>								
PQPFRPQQPYPK	<u>1799</u>								

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Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
QFLGQQPFPPQ	<u>1800</u>								
FLGQQPFPPQ	<u>1801</u>								
LGQQPFPPQ	<u>1802</u>								
QFLGQQPFPP	<u>1803</u>								
QFLGQQPF	<u>1804</u>								
IRNLALQTLPAMCN									
VY	<u>1805</u>								
NLALQTLPAMCNV									
Y	<u>1806</u>								
LALQTLPAMCNVY	<u>1807</u>								
IRNLALQTLPAM	<u>1808</u>								
IRNLALQTLP	<u>1809</u>								
EGDAFELTVSCQG				572	3578				
GLPK	<u>1810</u>								
ESTGMTPEKVPVSE		>50000	>47368.42	510	>71428.57		>31250		
VMGT	<u>1811</u>								
FPTIPLSRLFDNASL	<u>1812</u>	8071	114611	228	22	7210	3175	4969	9876
RLFDNASLRAHRL		89	97	77	2043	10328	1921	14985	23832
HQ	<u>1813</u>								
LRAHRLHQLAFDT		162	15603	5076	2197	10139	123	5621	15115
YQ	<u>1814</u>								
QLAFDTYQEFEEA		>20491.8	7981	>10738.2	33446	5399	2580	>33333.33	>59523.81
YI	<u>1815</u>			6					
QEFEEAYIPKEQKY		>20491.8	>171755.73	>21276.6	>88339.22	395	31344	>33333.33	>59523.81
S	<u>1816</u>								
IPKEQKYSFLQNPQ		128	49978	217	3633	9.0	8305	13553	79800
T	<u>1817</u>								
SFLQNPQTSLCFSES	<u>1818</u>	595	8617	6376	16880	>25832.77	48620	>33333.33	93856
TSLCFSESIPTPSNR	<u>1819</u>	604	182762	48	229	852	1064	>33333.33	4395
REETQQKSNELELR		8921	91054	9341	1324	1433	51179	22467	9680
I	<u>1820</u>								
SNLELLRISLLLIQS	<u>1821</u>	72	43487	621	189	379	642	>33333.33	3422
ISLLLIQSWLEPVQF	<u>1822</u>	184	27922	885	177	0.86	83	>33333.33	6247
SWLEPVQFLRSVFA		11	167103	1128	152	883	589	3416	3998
N	<u>1823</u>								
FLRSVFANSLVYGA		4.3	15221	6.7	43	59	16	13436	15127
S	<u>1824</u>								
NSLVYGASDSNVY		7313	81158	190	1585	1055	201	>33333.33	3896
DL	<u>1825</u>								
SDSNVYDLLKDLE		24369	54982	11032	>25680.53	95	182355	>33333.33	>59523.81
EG	<u>1826</u>								
GIQTLMGRLEDGSP		98	>55900.62	11914	2458	3745	18952	>33333.33	37821
R	<u>1827</u>								
RLEDGSPRTGQIFK		15693	76675	7906	1729	22125	35120	>33333.33	>59523.81
Q	<u>1828</u>								
RTGQIFKQTYSKFD		1555	20341	1680	1831	40	46	16432	8515
T	<u>1829</u>								
QTYSKFDTNSHND		17352	>55900.62	97	11218	78	54569	7726	31341
DA	<u>1830</u>								
TNSHNDALLKNY		16457	26397	20308	>25680.53	16329	245523	>33333.33	>59523.81
GL	<u>1831</u>								
ALLKNYGLLYCFR		137	9819	446	1286	551	11915	>33333.33	676
KD	<u>1832</u>								
DMDKVETFLRIVQ		1277	4813	867	1135	622	10484	1673	16127
CR	<u>1833</u>								
FLRIVQCRSVEGSC		106	33536	185	164	191	7199	7262	5311
GF	<u>1834</u>								
FPTIPLSRLFDNAM		6923	46707	9458	175	923	5529	1051	14964
L	<u>1835</u>								
RLFDNAMLRAHRL		2.3	27	6289	1520	4247	3297	212	>59523.81
HQ	<u>1836</u>								
QLAFDTYQEFEQNP		>17985.61	7851	28586	47399	4843	21064	>33333.33	>59523.81
Q	<u>1837</u>								

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Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
SFLQNPQTSLCCFR K	<u>1838</u>	106	1829	671	1816	1230	7026	7069	3082
SNLELLRICLLLIQS	<u>1839</u>	731	61913	1526	2303	1112	1222	19782	3970
ICLLLIQSWLEPVQF	<u>1840</u>	8511	50874	11303	5708	71	643	>33333.33	>59523.81
NSLVYGASDSNIYD L	<u>1841</u>	13068	>51428.57	240	3683	1229	297	>33333.33	>59523.81
SDSNIYDLLKDLEE G	<u>1842</u>	>17985.61	124500	17458	25922	137	>85034.01	>33333.33	50134
DKVETFLRIVQCCG F	<u>1843</u>	953	18325	1158	259	397	697	581	4080
SFLQNPQTSLTFSSES	<u>1844</u>	1191	2395	7780	15527	9558	6197	>33333.33	17714
TSLTFSESIPTSNR	<u>1845</u>	182	17425	18	98	686	682	17602	2461
ALLKNYGLLYTFR KD	<u>1846</u>	19	5982	160	266	303	5923	3616	2628
LLYTFRKDMDKVE TF	<u>1847</u>	>17985.61	23871	10623	17771	1133	53362	10448	>59523.81
DMDKVETFLRIVQ TR	<u>1848</u>	1111	11194	2030	133	454	436	183	51511
FLRIVQTRSVEGST GF	<u>1849</u>	6.4	3944	11	16	99	9.8	445	778
HLDMLRHLYQGCG VV	<u>1850</u>	304	37552	9417	2741	3593	27027	5384	12508
RLRIVRGTLFEDN YAL	<u>1851</u>	4.8	11287	8389	2929	1024	12	6325	1834
GVGSPYVSRLGIC L	<u>1852</u>	19	167949	1570	49	4156	190	1317	2614
TLERPKTSLSPGKNG V	<u>1853</u>	10103	134367	>22471.91	103285	>28592.93	25988	>75384.62	>300000
KIFGSLAFLPESFDG DPA	<u>1854</u>	597	74162	1195	1897	37	377	>75384.62	15796
ELVSEFSRMARDPQ	<u>1855</u>	201	1026	120	4882	15120	21259	4082	91575
GEALSTLVNLRLK VG	<u>1856</u>	719	11783	3045	305	14802	3191	192	20167
AYVLLSEKKISSIQS	<u>1857</u>	78	136	943	359	9471	3848	27	3338
VASLLTTAEVVVTE I	<u>1858</u>	604	136308	7431	810	6517	369	>118357.49	1955
KCEFQDAYVILLSE KK	<u>1859</u>	14	5791	73	943	351	336	489	185
ALSTLVNLRLKVG LQ	<u>1860</u>	49	153	517	31	2167	647	4.0	2166
MSYNLLGLFQRSS NC	<u>1861</u>	115	156715	366	1584	788	1060	3421	3646
LGFLQRSSNCQCQ KL	<u>1862</u>	437	112406	120	401	827	767	218	3729
RSSNCQCQKLLWQ LN	<u>1863</u>	9665	>191897.65	1046	2987	12652	9689	4530	74405
QCQKLLWQLNGRL EY	<u>1864</u>	181	133472	360	460	1004	3702	2519	4669
LWQLNGRLEYCLK DR	<u>1865</u>	1108	2356	816	8882	1024	10586	>16333.33	5206
GRLEYCLKDRRNF DI	<u>1866</u>	9854	853	918	4155	3238	12108	1318	25159
RNFDIPEEIKQLQQF	<u>1867</u>	6969	26262	18107	5375	>114457.83	47893	>144117.65	>77319.59
PEEIKQLQQFQKED A	<u>1868</u>	1026	40154	1618	618	7875	49505	11908	>77319.59
QLQQFQKEDAAVT IY	<u>1869</u>	85	17383	231	27473	1121	500	4862	55351
QKEDAAVTIYEML QN	<u>1870</u>	8376	>156521.74	9437	75877	785	45455	>144117.65	5989
AVTIYEMLQNIFAIF	<u>1871</u>	17	23730	101	808	163	267	6873	4540
EMLQNIFAIFRQDS S	<u>1872</u>	395	9544	685	689	456	3313	10429	9738
IFAIQRQDSSSTGW N	<u>1873</u>	132	402	9.6	71	118	1186	4725	970
RQDSSSTGWNETIV E	<u>1874</u>	>102040.82	38681	4637	184507	40847	36320	15135	9075

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STGWNETIVENLLA N	1875	21407	>156521.74	1755	10422	7060	3960	>144117.65	>77319.59
ETIVENLLANVYHQ R	1876	659	40053	789	802	326	21681	>144117.65	8151
NLLANVYHQRNHL KT	1877	152	40328	1039	1440	1492	8000	453	4160
VYHQRNHLKTVLE EK	1878	617	3135	7757	76003	153	6180	2101	>77319.59
LEKEDFTRGKRMS SL	1879	21965	50733	>20887.73	93968	5694	946	804	>77319.59
FTRGKRMSLHLK RY	1880	13	3302	1013	970	484	136	553	10925
RMSSLHLKRYYGRI L	1881	275	2181	993	4793	34	283	277	14964
HLKRYYGRIHLHYL KA	1882	26	3709	135	666	86	214	237	2896
YGRILHYLKAKEDS H	1883	30	42429	2343	917	23	900	704	7577
HYLKAKEDSHCAW TI	1884	1128	34758	2064	12153	3701	581	34851	>77319.59
KEDSHCAWTIVRV EI	1885	4835	>46656.3	353	1090	74	30	40000	2937
CAWTIVRVEILRNF Y	1886	66	3561	158	640	135	746	43672	757
VRVEILRNFYVINR L	1887	1.8	429	140	47	18	14	3585	485
RNFYVINRLTGYL R N	1888	1.7	2199	219	4618	182	527	167	7600
MSYNLLGFLQRSS NT	1889	25	107838	1152	813	433	8867	900	8972
LGFLQRSSNTQTQK L	1890	142	26455	18	211	1068	420	939	1345
RSSNTQTQKLLWQ LN	1891	10515	44338	2139	15497	12590	27678	1283	>77319.59
QTQKLLWQLNGRL EY	1892	32	3555	55	35283	86	3099	2042	2083
LWQLNGRLEYTLK DR	1893	698	511	757	16171	94	20198	43286	16619
GRLEYTLKDRRNF DI	1894	7252	30	3228	97035	1379	4961	4917	>77319.59
HYLKAKEDSHTAW TI	1895	232	70237	553	10677	15067	801	8526	10140
KEDSHTAWTIVRV EI	1896	1909	44754	746	2178	302	35	>79032.26	6079
TAWTIVRVEILRNF Y	1897	7.8	2997	44	84	115	29	57243	404
LGFLQRSSNCQSQK L	1898	192	4888	8.1	93	228	305	405	13167
RSSNCQSQKLLWQ LN	1899	2050	57946	595	16721	4010	8922	6943	4062
QSQKLLWQLNGRL EY	1900	127	33374	84	741	55	1166	991	5920
GIVEQCCTSICSLY Q	1901	11123	777105	10911	2995	17793	>79872.2	>10047.16	13855
TSICSLYQLENYCN	1902	11391	>154109.59	20462	3791	12457	>85616.44	>54444.44	>63025.21
GILEQCCTSICSLYQ	1903	11025	>187500	14862	5106	15983	54113	>54444.44	16714
GIVEQTTTSITSLYQ	1904	6354	107486	121	115	818	788	>54444.44	13304
EQTTTSITSLYQLE N	1905	18953	>143769.97	170	258	272	2230	>54444.44	17381
TSICSLYQLENYCG	1906	1125	202253	8841	1986	1089	247525	>54444.44	>83333.33
TSITSLYQLENYTN	1907	1253	81293	1468	138	851	6055	26791	9947
TSITSLYQLENYTG	1908	1132	96727	1628	129	115	8371	14562	46268
GIVEQCCCGSHLVE A	1909	10043	>74750.83	19904	2892	6626	41276	>54444.44	>63025.21
SLYQLENYCCGER GF	1910	3568	54469	7313	1527	2356	12308	>54444.44	>83333.33
CCTSICSLYQLENY CC	1911	11655	71239	8383	1604	629	35604	>54444.44	29845

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Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
GSHLVEALYLVC		194	>59681.7	2280	11512	2509	302	>54444.44	37166
N	<u>1912</u>								
CCGSHLVEALYLV		880	>55693.07	10081	20487	5230	1822	>54444.44	>63025.21
CC	<u>1913</u>								
FVNQHLCGSHLVE		583	>187500	19209	39746	>20663.4	6791	>54444.44	>63025.21
AL	<u>1914</u>								
QHLCGSHLVEALY		170	48557	12954	4303	9825	86	>54444.44	7422
LV	<u>1915</u>								
GSHLVEALYLVCG		525	>187500	8292	1603	4609	560	>54444.44	5386
ER	<u>1916</u>								
VEALYLVCGERGF		76	17558	209	124	1044	3869	24623	2233
FY	<u>1917</u>								
YLVCGERGFYTPK		11063	37210	1439	22980	730	64644	>54444.44	1520
T	<u>1918</u>								
FVNQHLCGSDLVE		117	>74750.83	19154	36693	14913	38662	>54444.44	>63025.21
AL	<u>1919</u>								
FVNQHLTGSHLVE		9.2	67240	858	14916	1065	15	>54444.44	41482
AL	<u>1920</u>								
QHLTGSHLVEALY		9.3	50338	>16096.5	3952	7423	38	>54444.44	42312
LV	<u>1921</u>			8					
GSHLVEALYLVGT		645	>176470.59	15781	1693	14443	553	>54444.44	>63025.21
ER	<u>1922</u>								
VEALYLVCGERGS		88	9972	833	194	6108	6485	>54444.44	6311
FY	<u>1923</u>								
VEALYLVCGERGF		14	11587	167	31	1027	5351	10565	3063
LY	<u>1924</u>								
VEALYLVGTGERGFF		9.9	2011	60	23	2342	195	1224	683
Y	<u>1925</u>								
YLVCGERGFLYTP		155	2033	>20460.3	>38550.5	>30134.81	12842	>54444.44	124
KT	<u>1926</u>			6					
YLVCGERGFYTD		17260	11790	>20460.3	>38550.5	>30134.81	92272	>54444.44	317
KT	<u>1927</u>			6					
YLVCGERGFYTKP		3207	42139	>20460.3	>38550.5	>30134.81	969	>54444.44	1673
T	<u>1928</u>			6					
YLVGTGERGFYTPK		779	517	>20460.3	>38550.5	30457	7737	29236	6295
T	<u>1929</u>			6					
YLVGTGERGFYTD		3259	7326	>20460.3	>38550.5	>30134.81	5328	>25789.47	2909
KT	<u>1930</u>			6					
YLVGTGERGFYTKP		1152	4801	>20460.3	>38550.5	>30134.81	78	4304	195313
T	<u>1931</u>			6					
VCGERGFYTPKTR		9622	1989	>20460.3	>38550.5	>15103.34	5494	419	14379
R	<u>1932</u>			6					
VTGERGFYTPKTR		18906	3018	7226	147000	13417	27824	9407	>300000
R	<u>1933</u>								
MWDLVLSIALSVG		205		1846			3032	23046	1727
CT	<u>1934</u>								
DLVLSIALSVGCTG		1197		13038			4029	>245000	2200
A	<u>1935</u>								
HPQWVLTAAHCLK		22	1103	875			563	1693	822
KN	<u>1936</u>								
QWVLTAAHCLKK		895		>40000			3402	98000	4813
NSQ	<u>1937</u>								
GQRVPVSHSFPHP		1563		>40000			629	>245000	102
LY	<u>1938</u>								
RVPVSHSFPHPLYN		67		>16000			101	100021	97
M	<u>1939</u>								
PHPLYNMSLLKHQ		19079		819			20691	3315	1592
SL	<u>1940</u>								
HPLYNMSLLKHQS		232	13007	499			1282	382	199
LR	<u>1941</u>								
NMSLLKHQSLRPD		3131		>40000			20620	26496	96825
ED	<u>1942</u>								
SHDLMLLRLSEPAK		56	2396	2244			106	1327	112
I	<u>1943</u>								
HDLMLLRLSEPAKI		16	1406	3063			109	544	43
T	<u>1944</u>								
PEEFLRPRSLQCVS		2001		>26666.6			5156	2207	5839
L	<u>1945</u>			7					
PRSLQCVSLHLLSN		1111		16000			2217	6107	28307
D	<u>1946</u>								

HLA-DR SUPERTYPE									
Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
NGVLQGITSWGPEP C	<u>1947</u>	1093		8433			2285	52234	50111
KPAVYTKVVHYRK WI	<u>1948</u>	5000		1433			2401	53	3677
LHLLSNDMCARAY SE	<u>1949</u>	2104	938	4277			27685	50230	59904
VGNWQYFFPVIFSK A	<u>1950</u>	37		4.1			100		
ESEFQAALSRKVA KL	<u>1951</u>			579	29617				
IGHLYIFATCLGLS YDGL	<u>1952</u>			>816.33	12199				
VGNWQYFFPVIFSK ASDSLQLVFGIELM EVD	<u>1953</u>			654	3846				
PAYEKLSAEQSPPP Y	<u>1954</u>			479	>250000				
RNGYRALMDKSLH VGTQCALTRR	<u>1955</u>			512	5779				
FFKNIVTFFKNIVT	<u>1956</u>	50000		>666.67	500000		>12500		
YKSAHKGFGKVDA QGTLSKI	<u>1957</u>	70	>900000	889	25000		108		
VDAQGTLSKIFKLG GRDSRS	<u>1958</u>	25	1383	1600	314		1171		
AC- ASQKRPSQRHGSK YLATAST	<u>1959</u>	50000	>900000	889	25000		2362		
ENPVVHFFKNIVTP R	<u>1960</u>								
ENPVVAFFKNIVTP R	<u>1961</u>								
ENPVVHAFKNIVTP R	<u>1962</u>								
ENPVVHFFANIVTP R	<u>1963</u>								
ENPVVHFFKNIVTP A	<u>1964</u>								
NPVVHFFKNIVT	<u>1965</u>								
HFFKNIVTPRTPPY	<u>1966</u>								
NPVVHFFKNIVTPR	<u>1967</u>								
LPVPGVLLKEFTVS GNILTI	<u>1968</u>	57	15058	14	12	12	57		
WITQCFLPVFLAQF PSGQRR	<u>1969</u>	679	25534	88	2804	216	74162		
DHRQLQLSISSCLQ QLSLLM	<u>1970</u>	1356	42666	1322	210	725	736		
YLAMPFATPMEAE LARRSLA	<u>1971</u>	46	46591	266	814	405	526		
AAPLLLARAASLSL G	<u>1972</u>	6.8	35410	139			160	30	64
APLLLARAASLSLG F	<u>1973</u>	8.4	56250	202			59	76	124
PLLLARAASLSLGF L	<u>1974</u>	10	>81818.18	521			162	37	58
SLSLGFLLFFWL D	<u>1975</u>	11417		4711			22727	>122500	24620
LLFFWLDRSVLAK EL	<u>1976</u>	2.9	6.3	2.6			135	163	518
DRSVLAKELKFVTL V	<u>1977</u>	705		569			2016	15815	4719
AKELKFVTLVFRH GD	<u>1978</u>	787	30000	783			606	1953	2355
RSPIDTFPTDPIKES	<u>1979</u>	>50000		13095			>62500	>245000	6124
FGQLTLGMEQHY EL	<u>1980</u>	2259		3210			>62500	109567	>187500
DRTLMSAMTNLAA LF	<u>1981</u>	97	64286	13			383	2362	222
MSAMTNLAALFPP	<u>1982</u>	1757		700			36084	73870	>187500

HLA-DR SUPERTYPE									
Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
EG									
MTNLAALFPPEGVS		24		>40000			>125000	39231	22822
I	<u>1983</u>								
PEGVSIWNPILLWQ		111		1778			15030	28577	103096
P	<u>1984</u>								
GVSIWNPILLWQPI		44	56250	10328			4992	11008	3985
P	<u>1985</u>								
WNPILLWQPIPVHT		208	>81818.18	695			521	115494	607
V	<u>1986</u>								
NPILLWQPIPVHTV		31	>81818.18	206			41	12999	575
P	<u>1987</u>								
PILLWQPIPVHTVPL		44	>81818.18	258			46	21244	168
P	<u>1988</u>								
ILLWQPIPVHTVPLS		45	>81818.18	170			19	13091	131
P	<u>1989</u>								
WQPIPVHTVPLSED		6386		>26666.6			159	>81666.67	17518
Q	<u>1990</u>			7					
LSGLHGQDLFGIWS		148		>26666.6			>35714.29	>81666.67	>125000
K	<u>1991</u>			7					
YDPLYCESVHNFTL		1597	16625	8889			838	30867	643
P	<u>1992</u>								
LPSWATEDTMTKL		20274		973			>35714.29	>81666.67	>125000
RE	<u>1993</u>								
LRELSLSLLSLYGI		655		371			4010	9368	1614
L	<u>1994</u>								
SELSLSLYGIHK		482	>81818.18	1549			20906	1186	1450
Q	<u>1995</u>								
LSLLSLYGIHKQKE		656	>81818.18	4444			>35714.29	1637	4959
K	<u>1996</u>								
KSRLQGGVLVNEIL		362		>26666.6			2838	>81666.67	5516
N	<u>1997</u>			7					
GGVLVNEILNHMK		2165	700	359			29463	3239	54411
RA	<u>1998</u>								
IPSYKKLIMYSAHD		9.9	9728	510			1946	60	351
T	<u>1999</u>								
YKKLIMYSAHDTT		17	22678	207			292	309	107
VS	<u>2000</u>								
LIMYSAHDTTVSGL		4496		24			731	24812	813
Q	<u>2001</u>								
DTTVSGLQMALDV		171		4424			14706	>245000	2876
YN	<u>2002</u>								
ALDVYNGLLPPYA		18		485			>83333.33	588	86603
SC	<u>2003</u>								
LDVYNGLLPPYAS		15		348			>83333.33	404	31277
CH	<u>2004</u>								
YNGLLPPYASCHLT		42		6189			>83333.33	14027	8022
E	<u>2005</u>								
FAELVGPVIPQDWS		12		4690			24056	>245000	39472
T	<u>2006</u>								
TVPLSEDQLLYLPF		4012	332	10755			11313	42162	37369
R	<u>2007</u>								
LTELYFEKGEYFVE		2249	592	8051			13062	18841	26949
M	<u>2008</u>								
GPVIPQDWSTECM			52098						
TT	<u>2009</u>								
QAHSLERVCHCLG		50000		667	500000		>250000		
KWLGHDPK	<u>2010</u>								
WTTCQSIAFPSKTS			17308	22					
ASIGSL	<u>2011</u>								
QKGRGYRGQHQA			>47368.42	88					
HSLERVCH	<u>2012</u>								
AATYNFAVLKLMG			>52941.18	533					
RGTKF	<u>2013</u>								
VATGLCFFGVALFC			>112500	351					
GCGHEA	<u>2014</u>								
FLYGALLLAEGFYT									
TGAVRQ	<u>2015</u>								
SAVPVYIYFNTWTT									
CQSIAF	<u>2016</u>								
TLSVTWIGAAPLIL		3.1	>81818.18	7273			16	840	5.4
S	<u>2017</u>								

HLA-DR SUPERTYPE									
Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
SVTWIGAAPLILSRI	<u>2018</u>	4.1	>81818.18	3152			83	139	30
VTWIGAAPLILSRIV	<u>2019</u>	8.1	>81818.18	8000			195	731	82
SQPWQVLVASRGR		66	>81818.18	7628			385	386	621
AV	<u>2020</u>								
GRAVCGGVLVHPQ		386		>26666.6			3582	>245000	8069
WV	<u>2021</u>			7					
GVLVHPQWVLTA		87	21320	67			153	1931	365
HC	<u>2022</u>								
HPQWVLTAACIR		13	3632	1621			283	1305	107
NK	<u>2023</u>								
QWVLTAACIRNK		50		19403			214	2598	967
SV	<u>2024</u>								
AHCIRNKSVILLGR		578	29704	69			2573	104	715
H	<u>2025</u>								
SVILLGRHSLFHP		717	1400	12649			26088	500	5216
D	<u>2026</u>								
VILLGRHSLFHPED		273	8744	8208			30625	737	18520
T	<u>2027</u>								
GQVFQVSHSFPHP		288	45000	8.2			27	548	33
Y	<u>2028</u>								
VFQVSHSFPHPYD		16	>75000	25			51	8751	17
M	<u>2029</u>								
PHPLYDMSLLKNR		1315		20787			10699	29813	12836
FL	<u>2030</u>								
SHDMLRLRLSEPAE		532	6215	4051			58	3538	64
L	<u>2031</u>								
HDLMLRLRLSEPAEL		62	2867	6193			152	3914	22
T	<u>2032</u>								
TDVAVKVMDLPTQE		>50000		>80000			>41666.67	20875	>107142.8
PA	<u>2033</u>								6
LHVISNDVCAQVH		789	8318	790			17451	>122500	32671
PQ	<u>2034</u>								
CAQVHPQKVTKFM		10206		2566			32275	8731	34893
LC	<u>2035</u>								
GGPLVCNGVLQGIT		3353		68			>35714.29	9334	16308
S	<u>2036</u>								
GPLVCNGVLQGITS		1724		30			4893	4187	32640
W	<u>2037</u>								
NGVLQGITSWGSEP		945	24942	560			485	5874	819
C	<u>2038</u>								
RPSLYTKVVHYRK		6041	53785	339			652	39	5484
WI	<u>2039</u>								
HSLFHPEDTGQVFQ			65260						
V	<u>2040</u>								
PRWLCAGALVLAG		46		>20000			766	26531	1439
GF	<u>2041</u>								
LGFLFGWFIKSSNE		10	>75000	1338			2261	1421	1701
A	<u>2042</u>								
LDELKAENIKFLY		1136	1370	4842			7470	1248	12778
N	<u>2043</u>								
IKKFLYNFTQIPHL		449	8080	43			29	512	160
A	<u>2044</u>								
KFLYNFTQIPHLA		340	13805	217			30	415	54
T	<u>2045</u>								
WKEFGLDSELAH		1139	85	96			3511	19971	7052
YD	<u>2046</u>								
LAHYDVLLSYPNK		79	37533	1117			3617	415	1009
TH	<u>2047</u>								
GNEIFNTSLFEPPPP		20412		>20000			>35714.29	>163333.33	10415
GKVFRGNKVKNAQ	<u>2048</u>								
LA		612		1087			2350	4121	31277
GNKVKNAQLAGA	<u>2049</u>								
KG		677		13333			>83333.33	28904	7882
GV	<u>2050</u>								
EYAYRRGIAEAVG		5.1		213			70	596	67
LP	<u>2051</u>								
AEAVGLPSIPVHPIG		5.4		9923			2015	>490000	23102
AVGLPSIPVHPIGY	<u>2052</u>								
Y	<u>2053</u>	3.6		4193			1080	4432	15377

HLA-DR SUPERTYPE									
Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
IGYYDAQKLEKM		1923		12649			>83333.33	8236	47246
GG	<u>2054</u>								
TGNFSTQKVKMHI		11180		833			9407	10282	1450
HS	<u>2055</u>								
TRIYNVIGTLRGAV		14	33333	6.3			4806	70	2900
E	<u>2056</u>								
ERGVAYINADSSIE		2440		6761			34021	>163333.33	25516
G	<u>2057</u>								
GVAYINADSSIEGN		1054		146			6244	23360	3048
Y	<u>2058</u>								
DSSIEGNYTLRVDC		16667		3360			14458	>163333.33	>187500
T	<u>2059</u>								
NYTLRVDCPLMY		6804	45	9.9			24597	6323	48412
SL	<u>2060</u>								
CTPLMYSLVHNL		93	19437	245			140	223	249
KE	<u>2061</u>								
DFFVFFQRLGIASG		143		221			21926	122	2005
R	<u>2062</u>								
EVFFQRLGIASGRA		28	>75000	22			5311	6.3	2976
R	<u>2063</u>								
TNKFSGYPLYHSV		3402		5521			30853	614	741
YE	<u>2064</u>								
YDPMFKYHLTVAQ		9.0	>75000	19			158	172	179
VR	<u>2065</u>								
DPMFKYHLTVAQV		5.7	>75000	9.1			168	43	258
RG	<u>2066</u>								
MFKYHLTVAQVRG		16	29032	18			72	70	266
GM	<u>2067</u>								
KYHLTVAQVRGG		137	33658	806			228	1519	5860
MVF	<u>2068</u>								
VAQVRGGMVFELA		228		662			4449	>98000	499
NS	<u>2069</u>								
RGGMVFELANSIVL		10	37118	229			41	8682	33
P	<u>2070</u>								
GMVFELANSIVLPF		15	4604	230			30	4995	81
D	<u>2071</u>								
VFELANSIVLPFDC		19	667	999			39	36123	50
R	<u>2072</u>								
ADKIYSISMKHPQE		22361		5310			4098	1136	3512
M	<u>2073</u>								
IYSISMKHPQEMKT		8452		16000			11573	1357	12293
Y	<u>2074</u>								
PQEMKTYSVSFDL		15143		3024			1192	>98000	1981
F	<u>2075</u>								
TYSVSFDSLFSVAVK		219	101	73			346	2256	526
N	<u>2076</u>								
VLRMMNDQLMFL		118	183	29			17334	1700	10684
ERA	<u>2077</u>								
LRMMNDQLMFLE		2704		392			17507	2492	4601
AF	<u>2078</u>								
RHVIYAPSSHNKYA		2174		481			31250	11667	481
G	<u>2079</u>								
RQIYVAAFTVQAA		3.7	28347	1.2			292	36	91
AE	<u>2080</u>								
QIYVAAFTVQAAA		1.6	26609	1.6			324	102	65
ET	<u>2081</u>								
VAAFTVQAAAETL		14	>75000	58			793	1420	127
SE	<u>2082</u>								
YISIINEDGNEIFNT		498	397	624			23719	>122500	83056
ISIINEDGNEIFNTS	<u>2083</u>								
		507	559	>12965.9			>23105.36	>122500	>52337.75
	<u>2084</u>			6					
EDFFKLERDMKINC		2710	468	226			8550	1439	>52337.75
S	<u>2085</u>								
FFKLERDMKINCSG		4419	121	483			>23105.36	8109	>52337.75
K	<u>2086</u>								
GVILYSDPADYFAP		1566	17	7508			7848	106291	2473
G	<u>2087</u>								
GAAVVHEIVRSFGT			12409						
L	<u>2088</u>								
NSRLQERGVAYIN	<u>2089</u>	614	318	5089			7997	3224	2616

HLA-DR SUPERTYPE									
Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
A									
VAYINADSSIEGNY		4716	531	411			9745	105832	5467
T	<u>2090</u>								
DQLMFLERAFIDPL			>19667.83						
G	<u>2091</u>								
KSNFLNCYVSGFHP		2500	>900000	296	3125		8333		
SD	<u>2092</u>								
AC-						500000		>25000	
NPDAENWNSQFEIL									
EDAA	<u>2093</u>								
EYLILSARDVLAVV				508					
S	<u>2094</u>								
YKTIAVDEEARR	<u>2095</u>	50000	143	4000	500000		250000		
GEALSTLVVNKIRG		292	29687	1535	246	30057	2325	383	40840
T	<u>2096</u>								
PYILLVSSKVSTVK		1.1	106	64	13	136	38	12	134
D	<u>2097</u>								
EAVLEDPYILLVSS		34	479	233	172	681	933	1666	15032
K	<u>2098</u>								
IAGLFLTTEAVVAD		6.8	27189	13	106	67	230	3893	409
K	<u>2099</u>								
ALSTLVVNKIRGTF		75	274	648	40	3626	396	20	18035
K	<u>2100</u>								
MKHILYISFYFILVN	<u>2101</u>	5893		189		3385	1250	15558	
KSLSTNLPYGRTN		4226		690			50000		
L	<u>2102</u>								
HFFLFLLYILFLVK		337		260			42443	19641	
M	<u>2103</u>								
LFLLYILFLVKMNA		1160		283			4868	10869	
L	<u>2104</u>								
ILFLVKMNALRRLP		0.80		5.6			56	19	
V	<u>2105</u>								
MNALRRLPVICSFL	<u>2106</u>	2.1		13			488	265	
V									
SAFLESQSMNKIGD		549		113			523	21493	
D	<u>2107</u>								
LKELIKVGLPSFEN		99		163			542	1493	
L	<u>2108</u>								
FENLVAENVKPPK		56		2372			120215	>25025.54	
VD	<u>2109</u>								
PATYGIHPVLTSLF	<u>2110</u>	1.03		15			139	181	
YGIHPVLTSLFNK		6.0		2.0			60	793	
V	<u>2111</u>								
LLKIWKNYMKIMN		121		132			395	132	
HL	<u>2112</u>								
MTLYQIQVMKRNQ		1219		117			31053	166	
KQ	<u>2113</u>								
QKQVQMMIMIKFM		121		213			3618	182	
GV	<u>2114</u>								
MIMIKFMGVIIYIMII	<u>2115</u>	2905		312			68040	66150	
GVIYIMIISKMMR		10		22			476	137	
K	<u>2116</u>								
LYYLFNQHIKKELY		27		1324			10244	1771	
H	<u>2117</u>								
HFNMLKNKMQSSF		12		18			3225	185	
FM	<u>2118</u>								
LDIYQKLYIKQEEQ		2834		1492			>88339.22	1204	
K	<u>2119</u>								
QKKYIYNLIMNTQ		73		24			11942	13255	
NK	<u>2120</u>								
YEALIKLLPFSKRIR	<u>2121</u>	55		1839			3578	180	
ENEYATGAVRPFQ		4438		281			4970	17329	
AA	<u>2122</u>								
NYELSKKAVIFTPI		713		536			5498	141	
Y	<u>2123</u>								
QKILIKIPVTKNIIT	<u>2124</u>	993		303			534	2240	
KCLVISQVSNSDSY	<u>2125</u>	628		16			46383	17859	

HLA-DR SUPERTYPE									
Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
K									
SKIMKLPKLPISNG		824		6485			83674	110	
K	<u>2126</u>								
FIHFFTWTGTMFVPK		745		273			489	1699	
Y	<u>2127</u>								
LCNFKKNIIALLIIP	<u>2128</u>	9.7		312			423	21324	
KKNIIALLIIPPKIH	<u>2129</u>	13		203			495	157	
ALLIIPPKIHISIEL	<u>2130</u>	648		1738			8.4	11957	
SMEYKKDFLITARK		939		24			776	8897	
P	<u>2131</u>								
KSKFNILSSPLFNNF	<u>2132</u>	0.80		16			65	152	
FKKLKNHVLFLQM		2.3		28			11	695	
MN	<u>2133</u>								
KNHVLFLQMMNV		12		32			757	>120098.04	
NLQ	<u>2134</u>								
VLFQMMNVNLQ		6.3		30			8441	56770	
KQL	<u>2135</u>								
NVNLQKQLLTNHLI		96		2460			555	11245	
N	<u>2136</u>								
QKQLLTNHLINTPK		675		228			4412	20984	
I	<u>2137</u>								
NHLINTPKIMPHII	<u>2138</u>	1378		4798			625	1296	
YILLKKILSSRFNQ		220		183			8.3	18	
M	<u>2139</u>								
FNQMIFVSSIFISFY	<u>2140</u>	483		2091			854	16504	
KVSCKGSgyTFTA		5000		381	50000		2946		
YQMH	<u>2141</u>								
IAKVPPGPNITAEY		50000	>30000	>666.67	500000		>12500		
GDKWLD	<u>2142</u>								
TAEYGDKWLDKAS		50000	>30000	>666.67	16667		3125		
TWYGKPT	<u>2143</u>								
AKSTWYGKPTGAG		50000	>30000	667	500000		>12500		
PKDNGGA	<u>2144</u>								
GAGPKDNGGACGY		50000	>30000	>666.67	500000		>12500		
KDVKAP	<u>2145</u>								
FNGMTGCGNTPIFK		50000	51962	>666.67	500000		>12500		
DGRGCG	<u>2146</u>								
PIFKDGRGCGSCFEI		50000	6784	>666.67	500000		>12500		
KCTKP	<u>2147</u>								
SCFEIKCTKPESCSG		50000	>900000	>666.67	500000		12500		
EAVTV	<u>2148</u>								
AFGSMAKKGEEQN		50000	>30000	>666.67	50000		>12500		
VRSAGEL	<u>2149</u>								
TPDKLTGPFTVRYT		50000	>900000	>666.67	500000		>12500		
TEGGTK	<u>2150</u>								
VRYTTEGGTKSEV		50000	>30000	>666.67	500000		>12500		
EDVIEG	<u>2151</u>								
TCVLGKLSQELHK		26	29529	14848	7566	9001	18653	7656	17895
LQ	<u>2152</u>								
KLSQELHKLQTYPR		19	196889	19684	2076	12198	85464	28656	19129
T	<u>2153</u>								
LHLKQTYPRNTNTGS		2118	>205479.45	15182	9921	>7403.08	40226	1618	>29228.37
G	<u>2154</u>								
KLQTYPRNTNTGSGT		>10060.36	>205479.45	>26490.0	114672	>9806.45	>99206.35	>51578.95	>29228.37
P	<u>2155</u>			7					
CCVLGKLSQELHK		34	17387	19764	31253	5299	41656	5640	21704
LQ	<u>2156</u>								
CSNLSTCVLGKLSQ		296	>205479.45	14339	28603	5340	31837	3516	7225
E	<u>2157</u>								
TSNLSTTVLGKLSQ		298	86798	8016	32358	9280	31275	2058	2469
E	<u>2158</u>								
TTVLGKLSQELHKL		133	92782	22449	36802	>9806.45	26113	16182	23824
Q	<u>2159</u>								
DIAAKYKELGY	<u>2160</u>		>900000	>470.59					
ALVRQGLAKVA	<u>2161</u>	1250		190	500000				

HLA-DR SUPERTYPE									
Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
PATLIKAIDGDTVK		278	6429	296	3846		8333		
LMYKGQ	<u>2162</u>								
TPETKHPKKGVEK		>1000	>900000	>500	500000		12500		
YGPEASA	<u>2163</u>								
VEKYGPEASAFK		50000	>900000	1333	500000		12500		
KMVENAK	<u>2164</u>								
FTKKMVENAKKIE		>1000	11619	>500	500000		8333		
VEFDKGQ	<u>2165</u>								
YIYADGKMVNEAL		65		500	4167		1563		
VRQGLAK	<u>2166</u>								
HEQHLLKSEAQAK		50000	90000	80000	16667		6250		
KEKLNW	<u>2167</u>								
QAKKEKLNWSED		50000	>900000	364	3125		>250000		
NADSGQ	<u>2168</u>								
YFNNFTVSFWLRV		50000		615	25000				
PK	<u>2169</u>								
FSYFPSI	<u>2170</u>	50000		889	16667				
YSFFPSI	<u>2171</u>	50000		889	500000				
YSYFPSIR	<u>2172</u>	50000	>900000	667	16667		7217		
DPNANPNVDPNAN				738	>5494.51		>15625		
PNVNANPNANPNA									
NP(X4)	<u>2173</u>								
QKWAAVVVPS	<u>2174</u>	50000		1000	50000				
TWQLNGEELIQDM		50000		889	2273				
ELVETRPAG	<u>2175</u>								
PEFLEQRRRAVD		5000		80000	500000		250000		
YC	<u>2176</u>								
STORKUSP33				617	2069				
DYSYLQSDPDSFQ		>50000		189	>500000	>126666.67	>250000	>61250	>107142.8
D	<u>2178</u>			264	>500000	>126666.67	>250000	>61250	6
DFSYLQSDPDSFQ									
D	<u>2179</u>			195					6
QNILFSNAPLGPQF									
P	<u>2180</u>								
QNILLSNAPLVPQF				538					
P	<u>2181</u>								
DYSYLQSDPDSFQ				316	>166666.67				
D	<u>2182</u>								
KYVKQNTLKLAT	<u>2183</u>	9.9		6.2	25000				
P(X)KQNTLKLAT	<u>2184</u>	1.7							
EEDIEHPIQEEY	<u>2185</u>	>9057.97	>18549.05	>7518.8	12203	849	>6742.18		128305
HQAISPRTLNSPAIF	<u>2186</u>	1961	298315	6214	1314	3450	39701	14848	286179
YTDVFSLDPTFTIET			217						
T	<u>2187</u>								
YAGIRRDGLLLRLV			9.6						
D	<u>2188</u>								
LFFYRKSVWSKLQ		19	30163	913	1383	84	84	65	
SI	<u>2189</u>								
RPVNMDDYVVGAR		29	22	3.1	21	812	346	748	
TFRREKR	<u>2190</u>								
RPGLLGASVLGLD		1789	35768	6522	4414	3183	506	>61250	
DI	<u>2191</u>								
LYFVKVDVTGAYD		16	9.6	2.8	13	14	5892	413	
TI	<u>2192</u>								
FAGIRRDGLLLRLV		2381	3.6	7092	3820	>3365.21	41148	7650	
D	<u>2193</u>								
AKTFLRTLVRGVPE		104	54159	208	3326	105	25	9.2	
Y	<u>2194</u>								
YGAVVNLRKTVVN		13509	150175	4194	4531	>95000	8274	113	
FP	<u>2195</u>								
GTAQVQMPAHGLF		1.6	37275	8.1	34	18	90	99	
PW	<u>2196</u>								
WAGLLDTRTLEV		2016	22	49	323	1238	186	>61250	
QS	<u>2197</u>								
RTSIRASLTFNRGF		1430	256	770	177	5131	411	5475	
K	<u>2198</u>								

HLA-DR SUPERTYPE									
Sequence	SEQ ID NO.	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
RVIKNSIRLTL	<u>2199</u>	3650	584	9249	5389	80682	2239	1175	2566
PVIKNSIKLRL	<u>2200</u>	1549	198	34245	14612	277735	4091	541	2851
ATSTKKLHKEPATL	<u>2201</u>	4.6	8018	113	1020		2083		
IKAIDG									

TABLE 27

Sequence	SEQ ID NO.	HLA-DR SUPERTYPE						
		DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
AC-		>33333.33	>10000	200000	101		1250	
NPTKHKWEAAHVAEQ								
LAA	1543							
DDYVKQYTKQYTKQN		>1111.11			>11111.11		35	
TLKK	1544							
AAAKAAAAAAYAA	1545	200000			6250		2857	
AC-								
AAAKAAAAAAYAA	1546							
(20)AYA(20)A(20)A(20)K		200000					2857	
(20)A(20)	1547							
AC-AAAKATAAAAAAYAA	1548							
AC-AAAKAAAAAFAA	1549							
AC-								
AAAKATAAAAA(10)AA	1550							
AC-								
AAAKATAAAAA(23)AA	1551							
AAKAAAAAAA(10)AA	1552							
AAAYAAAAATAKAAA	1553							
AALAAAAAAKAAA	1554	2222					67	
AAEAAAAATAKAAA	1555							
AAYYJAAAAKAAA	1556							
AAAYAAAAJKAAA	1557							
AFLRAAAAAAFAA	1558							
AFLRQAAAAAFAAY	1559							
AAFAAAKTAAAF	1560	4.6			20000		25	6.4
YAAFAAAKTAAAF	1561	2.6			33333	30	9.5	
AALKATAAAAAA	1562							
YAR(15)ASQTTLKAKT	1563	3.9					3.6	
YARF(33)QTTLKAKT	1564							
PKYFKQRILKFAT	1565							
PKYFKQGFLKGAT	1566							
PKYGKQIDLKGAT	1567							
AAFFFFFGGGGA	1568							
AADFFFFFFDA	1569							
AAKGKIGFGIFA	1570							
AAFIGGGKIIKA	1571							
AAKIFIGFFIDGA	1572							
AAFIGFGKIKFIA	1573							
AAKIGFGIKIGFA	1574							
AAFKIGKFGIFFA	1575							
AADDDDDDDDDDA	1576							
(43)AAIGFFFFKKGIA	1577							
(43)AAFFGIFKIGKFA	1578							
(43)AADFGIFIDFIIA	1579							
(43)AAIGGIFIFKKDA	1580							
(43)AAFIGFGKIKFIA	1581							
(43)AAKIGFGIKIGFA	1582							
(43)AAFKIGKFGIFFA	1583							
AAAKAAAAAFAF	1584							

HLA-DR SUPERTYPE								
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
AAAKAAAAAAFA	<u>1585</u>							
AAAKAAAAAAFAA	<u>1586</u>							
AAAKAAAAFAAAA	<u>1587</u>							
FAAAAAAAAAAAAA	<u>1588</u>							
AAAAAAAAAAAAAAN	<u>1589</u>							
AAAAAAAAAAAAANA	<u>1590</u>							
AAANAAAAAAAAAAA	<u>1591</u>							
AAAAAAAAAAAAAAS	<u>1592</u>							
AAAAASAAAAAAA	<u>1593</u>							
ASAAAAAAA	<u>1594</u>							
AFAAAKTAA	<u>1595</u>							
YARFLALTTLRARA	<u>1596</u>							
YAR(15A)SQTTLKAKT	<u>1597</u>	2.5					1.4	48
YAR(15A)RQTTLKAAA	<u>1598</u>	1.2					0.94	62
(15A)RQTTLKAAA	<u>1599</u>	1.8					9.5	3095
(16A)RQTTLKAAA	<u>1600</u>	77					4000	
(46)AAKTAAFA	<u>1601</u>							
(39)AAAAATKAAA	<u>1602</u>							
(52)AAAAATKAAAA	<u>1603</u>							
(55)AAAAATKAAAA	<u>1604</u>							
A(14)AAAKTAAA	<u>1605</u>	43					120	
AA(14)A(35)ATKAAAA	<u>1606</u>							
AA(14)AA(36)TKAAAA	<u>1607</u>							
AFAAAKTAA(72)	<u>1608</u>							
(49)AAAKT(64)AAA	<u>1609</u>							
(49)AAAKTA(64)AA	<u>1610</u>							
HQAISPRTLNGPGPGSP	<u>1611</u>	9875	638	5570		232	32930	
AIF	<u>1612</u>							
YAAFAAAKTAAFA	<u>1613</u>				>4347.83			
TEGRCLHYTVDKSKPK	<u>1614</u>	>1250			4082		2857	
AWVAWRNRCK	<u>1615</u>	>5000			>11111.11		44	
IVSDGNGMNAWVAWR	<u>1616</u>	6667			>6250		>2222.22	
NRC	<u>1617</u>							
PHHTALRQAILSWGEL	<u>1618</u>	3116		5.3		48	261	
MTLA	<u>1619</u>	>10000			>7692.31		>5000	
WMYYHGQRHSDEHHH	<u>1620</u>	>6666.67			>33333.33		>10000	
YIVMSDWTGGA	<u>1621</u>	200000					200000	
AHAHAHAHAHAHAHA	<u>1622</u>							
A	<u>1623</u>							
MDIDPYKEFGATVELLS	<u>1624</u>		2415					
FLPSDFFP	<u>1625</u>							
GMLPVCPLIPGSSTTST	<u>1626</u>	2500			>25000		200000	
GP	<u>1627</u>	6667			1449		6667	
LGFFPDHQLDPAFRANT	<u>1628</u>	26	21	126		995	>11441.65	
GYKVLVLNPSV	<u>1629</u>	>23337.22	>2464.79	1934		11687	>12586.53	
LMAFTAAVTS	<u>1630</u>	342	>2569.75	>12709.5		>6608.93	25499	
TFALWRVSAEEY	<u>1631</u>	243	>6398.54	>15268.4		>7930	>35587.19	
ALWRVSAEEY	<u>1632</u>			6				
EEYVEIRQVGDFH	<u>1633</u>	4683	>1895.99	2060		2063	9754	
VGGVYLLPRRGPRLG	<u>1634</u>	88	>15350.88	4.2	60753	19239	12	

HLA-DR SUPERTYPE								
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
VGGAYLLPRRGPR LGV	<u>1629</u>	507	24663	4.1	>66533.6	37640	50	
VGGVALLPRRGPR LGV	<u>1630</u>	154	>15350.88	8.5	>66533.6	25688	20459	
VGGVYALPRRGPR LGV	<u>1631</u>	12	>15350.88	451	>66533.6	26122	34	
VGGVYLAPRRGPR LGV	<u>1632</u>	35	>15350.88	55	>66533.6	>42059.4 6	76	
VGGVYLLARRGPR LGV	<u>1633</u>	6.5	10325	2.8	17030	4338	17	
VGGVYLLPARGPR LGV	<u>1634</u>	694	201	6.5	18073	18960	40	
VGGVYLLRRAGPR LGV	<u>1635</u>	67	>15350.88	6.2	91912	30707	7.9	
GAPLGAARALAHGV	<u>1636</u>	24	8739	1615	>70972.32	3959	11983	
GAALGAARALAHGV	<u>1637</u>	168	19335	4483	>70972.32	3509	25372	
GAPLAGAARALAHGV	<u>1638</u>	9.5	7215	2810	>70972.32	2963	7688	
GAPLGAAARALAHGV	<u>1639</u>	36	15091	3920	>70972.32	16533	4502	
GAPLGGLARALAHGV	<u>1640</u>	12	76	1805	123762	3950	4256	
GAPLGGALRALAHGV	<u>1641</u>	83	340	2068	>51098.62	4889	5396	
GAPLGGAAAALAHGV	<u>1642</u>	43842	23810	7682	>51098.62	31	12916	
GAPLGGAAARLLAHGV	<u>1643</u>	80	29412	631	>51098.62	2549	26684	
GAPLGGAAARAAAHGV	<u>1644</u>	3633	>23489.93	>8666.67	>51098.62	41441	42463	
GAPLGGAAARALAAAGV	<u>1645</u>	45	23179	5714	>51098.62	3865	8354	
FPDWQNYTPGPTRF	<u>1646</u>	>51282.05	>12027.49	35058		33923	>20533.88	
RFPLTFGWCFKLVPV	<u>1647</u>	62289	4797	514		964	>20533.88	
RQDILDWVYHTQGY	<u>1648</u>	>51282.05	6775	723		1326	16155	
RQEILDWVYHTQGF	<u>1649</u>	11113	5384	985		1071	>20533.88	
LSHFLKEKGGLEGLI	<u>1650</u>	9460	>12027.49	>39737.9 9		18709	>20533.88	
LSFFLKEKGGLDGLI	<u>1651</u>	614	>12027.49	>39737.9 9		13214	15272	
LEPWNHPSQPKTACT	<u>1652</u>	>15325.67	>11041.01	2665		92	2939	
QVCFITKGLGISYGR	<u>1653</u>	31	92	3555		876	3950	
QLCFLKKGLGISYGR	<u>1654</u>	9.5	88	4212		282	1190	
PPEESFRFGEEKTTPS	<u>1655</u>	>10000			>14285.71		>2857.14	
CIVYRDGNPYAVCDK	<u>1656</u>	>14662.76	1646	650		>24786.3 2	>10666.67	
HYCYSLYGTTLEQQY	<u>1657</u>	12397	>13725.49	4849		1292	>10666.67	
CYSLYGTTLEQQYNK	<u>1658</u>	>14662.76	>13725.49	5060		189	>10666.67	
NTSLQDIEITCVYCK	<u>1659</u>	>14662.76	14857	678		11710	>10666.67	
VFEFAFKDLFVVYRD	<u>1660</u>	10923	7675	4871		18117	>10666.67	
EFAFKDLFVVYRDSI	<u>1661</u>	9496	9996	5355		9072	5998	
DLFVVYRDSIPHAAC	<u>1662</u>	1163	11172	2832		2676	10741	
FVVYRDSIPHAACHK	<u>1663</u>	1194	1851	349		18144	2343	
NTGLYNLLIRCLRCQ	<u>1664</u>	14	5692	67		222	598	
IRCLRCQKPLNPAEK	<u>1665</u>	>14662.76	>13725.49	6928		611	>10666.67	
PRKLHELSSALEIPY	<u>1666</u>	5990	51	1116		1710	>10666.67	
EIPYDELRLNCVYCK	<u>1667</u>	>18001.8	858	2084		9047	>62305.3	
TEVLDFAFDTLTIVY	<u>1668</u>	>18001.8	>13059.7	561		110	>62305.3	
VLDFAFTDLTIVYRD	<u>1669</u>	7474	3102	645		11294	14839	
DFAFTDLTIVYRDDT	<u>1670</u>	14334	5008	3651		21621	675	
TIVYRDDTPHGVCTK	<u>1671</u>	>18001.8	6280	5449		>21521.3 4	>62305.3	
WYRYSVYGTTLEKLT	<u>1672</u>	1670	805	421		1039	62	
ETTIHNIELQCVECK	<u>1673</u>	>18001.8	6282	11191		112	>62305.3	

HLA-DR SUPERTYPE								
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
SEVYDFAFADLTVVY	<u>1674</u>	>18001.8	>13059.7	955		1325	11802	
VYDFAFADLTVVYRE	<u>1675</u>	>18001.8	>13059.7	9446		10720	27275	
DFAFADLTVVYREGN	<u>1676</u>	>18001.8	9627	4915		17973	39785	
TVVYREGNPFGICKL	<u>1677</u>	>18001.8	>13059.7	13850		16200	48840	
GNPFGICKLCLRFLS	<u>1678</u>	1084	9737	1139		196	6594	
NYSVYGNTLEQTVKK	<u>1679</u>	>56657.22	8614	15587		>25108.2 3	14326	
KKPLNEILIRCIICQ	<u>1680</u>	1299	965	1870		140	26273	
NEILIRCIICQRPLC	<u>1681</u>	20827	7174	18927		883	>29761.9	
IRCIICQRPLCPQEK	<u>1682</u>	6757	7295	25349		510	15154	
CIVYRDCIAYAACHK	<u>1683</u>	35566	12898	3847		2578	1912	
NTELYNLLIRCLRCQ	<u>1684</u>	259	5674	2449		797	854	
IRCLRCQKPLNPAEK	<u>1685</u>	21581	>9641.87	27591		447	20171	
REVYKFLFTDLRIVY	<u>1686</u>	2263	80	258		203	155	
RIVYRDNNPYGVCIM	<u>1687</u>	3446	119	821		1403	20474	
NNPYGVCIMCLRFLS	<u>1688</u>	7786	4797	6662		207	7258	
EERVKKPLSEITIRC	<u>1689</u>	6877	8919	132		2990	7910	
IRCIICQTPLCPEEK	<u>1690</u>	5461	17444	9766		916	>51020.41	
EIPLIDLRLSCVYCK	<u>1691</u>	47355	6936	656		861	16853	
SCVYCKKELTRAEVY	<u>1692</u>	569	23385	4374		673	3197	
VCLLFYSKVRKYRY	<u>1693</u>	326	309	61		2343	182	
YYDYSVYGATLESIT	<u>1694</u>	9122	8923	1106		32378	>51020.41	
IRCYRCQSPLTPEEK	<u>1695</u>	6645	>14403.29	480		28659	>51020.41	
VYDFVFADLRIVYRD	<u>1696</u>	12168	79	855		4392	>51020.41	
DFVFADLRIVYRDGN	<u>1697</u>	6957	162	1253		6709	8433	
RIVYRDGNPFVAVCKV	<u>1698</u>	174	122	81		1606	3148	
GNPFAVCKVCLRLLS	<u>1699</u>	296	7389	117		126	657	
KKCLNEILIRCIICQ	<u>1700</u>	7579	731	3176		257	>9925.56	
NEILIRCIICQRPLC	<u>1701</u>	16056	10184	8177		372	>22909.51	
RTAMFQDPQERPRKL	<u>1702</u>	1034	17086	73192		20481	7474	
LFVVYRDSIPHAACH	<u>1703</u>	1582	697	437		3580	7854	
LTIVYRDDTPHGVCT	<u>1704</u>	15880	1852	27048		16993	>15267.18	
LCIVYRDCIAYAACH	<u>1705</u>	9886	5662	2269		2881	9738	
YKFLFTDLRIVYRDN	<u>1706</u>	10122	77	2912		1342	800	
YNFACTELKLVYRDD	<u>1707</u>	11615	10167	3082		12866	1673	
LKLVYRDDFPYAVCR	<u>1708</u>	698	699	1877		3828	9156	
YDFVFADLRIVYRDG	<u>1709</u>	6540	8173	25727		10907	11161	
LRIVYRDGNPFVAVCK	<u>1710</u>	109	123	169		1566	6820	
HEYMLDLQPETTDLY	<u>1711</u>	>56179.78	12990	30895		2099	>22909.51	
TLRLCVQSTHVDIRT	<u>1712</u>	17613	932	3957		243	>22909.51	
IRTLLEDLLMGTLGIV	<u>1713</u>	1156	789	2181		23	12385	
LEDLLMGTLGIVCPI	<u>1714</u>	8514	1693	229		1800	9475	
DLLMGTLGIVCPICS	<u>1715</u>	>56179.78	1053	1427		4123	16198	
KATLQDIVLHLEPQN	<u>1716</u>	25948	603	6968		159	>9925.56	
IDGVNHQHLPARRAE	<u>1717</u>	>56179.78	>11475.41	>36842.1 1		344	12573	
LRAFQQLFLNTLSFV	<u>1718</u>	106	1.01	20		2.2	253	
FQQLFLNTLSFVCPW	<u>1719</u>	10311	9.3	24792		309	17330	

HLA-DR SUPERTYPE								
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
QDYVLDLQPEATDLH		>11918.95	>11475.41	>62758.6		1851	>22909.51	
	<u>1720</u>			2				
DIRILQELLMGSFGI	<u>1721</u>	18982	5796	1625		16	>55096.42	
IRILQELLMGSFGIV	<u>1722</u>	7978	1038	294		17	>55096.42	
ELLMGSFGIVCPNCS	<u>1723</u>	>59171.6	933	1928		206	>55096.42	
KEYVLDLYPEPTDLY	<u>1724</u>	>59171.6	>14767.93	3171		476	>55096.42	
LRTIQQLMGTVNIV	<u>1725</u>	3641	6.4	265		15	32108	
IQQLMGTVNIVCPT	<u>1726</u>	11062	9.0	2010		166	>55096.42	
QLLMGTVNIVCPTCA		>59171.6	118	>38396.6		11550	>55096.42	
	<u>1727</u>			2				
RETLQEIVLHLEPQN	<u>1728</u>	7896	11360	16220		95	>55096.42	
LRTLQQLFLSTLSFV	<u>1729</u>	208	55	29		3.1	1994	
LQQLFLSTLSFVCPW	<u>1730</u>	11693	133	296		22	36943	
KDYILDLQPETDHLH		>17436.79	23654	>37448.5		490	>55096.42	
	<u>1731</u>			6				
LRTLQQMLLGTQV	<u>1732</u>	907	616	1697		88	>46620.05	
LQQMLLGTQVVC	<u>1733</u>	>31645.57	395	1266		1014	29198	
QMLLGTQVVC	<u>1734</u>	>31645.57	874	4144		258	>31446.54	
VPTLQDVVLELTPQT	<u>1735</u>	>31645.57	14985	12263		1000	>31446.54	
LQDVVLELTPQTEID		>31645.57	1145	>33090.9		1116	>31446.54	
	<u>1736</u>			1				
QDVVLELTPQTEIDL		>31645.57	10274	>33090.9		1719	>31446.54	
	<u>1737</u>			1				
CKFVVQLDIQSTKED	<u>1738</u>	>31645.57	>11437.91	22851		301	>31446.54	
VVQLDIQSTKEDLRV	<u>1739</u>	7353	708	5044		226	8690	
DLRVVQQLMGALTV	<u>1740</u>	667	57	132		9.5	10879	
LRVVQQLMGALTVT	<u>1741</u>	314	8.9	56		7.7	8755	
VQQLMGALTVTCPL	<u>1742</u>	11074	574	526		204	7151	
QQLMGALTVTCPLC	<u>1743</u>	7657	1223	4461		1470	>31446.54	
QLLMGALTVTCPLCA	<u>1744</u>	>31645.57	1817	3761		2224	>31446.54	
REYILDLHPEPTDLF		4152	13183	>33090.9		316	>31446.54	
	<u>1745</u>			1				
TCCYTCGTTVRLCIN	<u>1746</u>	8636	739	3820		891	16033	
VRTLQQLMGCTIV	<u>1747</u>	1409	37	1829		139	>15267.18	
LQQLMGCTIVCPS	<u>1748</u>	9447	753	2441		2667	>15267.18	
MLDLQPETDLYCYE		>15209.13	>12027.49	>48404.2		20	>15267.18	
	<u>1749</u>			6				
VLDLYPEPTDLYCYE	<u>1750</u>	>15209.13	>12027.49	21591		18	>15267.18	
LREYILDLHPEPTDL	<u>1751</u>	9827	12365	10949		2040	>40404.04	
HIEFTPTRTDYACRV	<u>1752</u>	200000			>7142.86		200000	
LWWWNNESLPVSPRL	<u>1753</u>							
YEEYVRFSDVGE	<u>1754</u>	200000					200000	
EEYVRFSDVGE	<u>1755</u>	200000					200000	
APRLICDSRVLERY	<u>1756</u>	>111111.11	149	1384	1617	2840	6087	
ICDSRVLERYLLEAK	<u>1757</u>	2945	20402	85	16159	8550	7295	
VLERYLLEAKEAENI	<u>1758</u>	17227	881	269	340	8920	6714	
EHCSLNENITVPDTK	<u>1759</u>	>111111.11	84	12013	8307	52943	6626	
NENITVPDTKVNIFYA	<u>1760</u>	17921	9338	22568	>38167.94	>38461.5	12214	
	<u>1761</u>					4		
VPDTKVNIFYAWKRME	<u>1762</u>	8861	14795	333	>38167.94	23602	449	
VNIFYAWKRMEVGQQA		50	14798	1194	22507	1490	455	
WKRMEVGQQA	<u>1763</u>	512	159	1812	>42194.09	238	4300	
Q								

HLA-DR SUPERTYPE								
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
VGQQAVEVWQGLALL	<u>1764</u>	>17241.38	1313	12	>38167.94	3901	>7785.13	
VEVWQGLALLSEAVL	<u>1765</u>	5157	4473	58	>38167.94	1334	13794	
GLALLSEAVLRGQAL	<u>1766</u>	2578	1216	1939	>38167.94	3.5	105	
SEAVLRGQALLVNSS	<u>1767</u>	3484	7.4	151	3997	23	1057	
RGQALLVNSSQPWEP	<u>1768</u>	7698	3.4	2876	6165	1554	558	
LVNSSQPWEPLQLHV	<u>1769</u>	>8163.27	504	2359	18044	3412	10039	
QPWEPLQLHVDKAVS	<u>1770</u>	8897	695	12480	1924	103	2929	
LQLHVDKAVSGLRSL	<u>1771</u>	910	53	2707	1044	31	76	
DKAVSGLRSLTTLR	<u>1772</u>	52	187	60	3150	2006	104	
GLRSLTTLRALGAQ	<u>1773</u>	3.7	871	6.2	12947	283	2.7	
TTLRALGAQKEAIS	<u>1774</u>	860	1512	89	33256	251	21	
ALGAQKEAISPPDAA	<u>1775</u>	4212	>12411.35	14216	>91743.12	27294	3963	
KEAISPPDAASAAPL	<u>1776</u>	601	9272	1201	27203	2988	310	
PPDAASAAPLRTITA	<u>1777</u>	2582	10205	1267	10584	182	1117	
SAAPLRTITADTFRK	<u>1778</u>	3883	809	858	2111	17	45	
RTITADTFRKLFVY	<u>1779</u>	166	95	35	672	1561	93	
DTFRKLFVYSNFLR	<u>1780</u>	11	10	0.95	43687	1029	26	
LFRVYSNFLRGKCLK	<u>1781</u>	173	80	2.8	8981	2333	2.9	
SNFLRGKCLKYTGEA	<u>1782</u>	192	4730	30	4075	2442	5.7	
KLKLYTGEACRTGDR	<u>1783</u>	>17241.38	880	130	17787	20089	636	
APPRLITDSRVLERY	<u>1784</u>	2750	92	238	710	2263	698	
ITDSRVLERYLLEAK	<u>1785</u>	5279	>14705.88	18	>42194.09	12401	621	
EHTSLNENITVPDTK	<u>1786</u>	>408163.27	13	11082	>42194.09	>29029.03	5547	
KLKLYTGEATRTGDR	<u>1787</u>	4364	841	18	5298	14838	731	
PQPFRPQQPYYPQ	<u>1788</u>					15		
PFRPQQPYYPQ	<u>1789</u>					42		
PQPFRPQQPYYP	<u>1790</u>					14		
PQPFRPQQP	<u>1791</u>					19		
KQPFRPQQPYYPQ	<u>1792</u>					56		
PKPFRPQQPYYPQ	<u>1793</u>					3.4		
PQPFRPQQPYYPQ	<u>1794</u>					19		
PQPFRKQQPYYPQ	<u>1795</u>					22		
PQPFRPQKPYPQ	<u>1796</u>					22		
PQPFRPQQPKPQ	<u>1797</u>					325		
PQPFRPQQPYKQ	<u>1798</u>					35		
PQPFRPQQPYPK	<u>1799</u>					22		
QFLGQQQPFPPQ	<u>1800</u>					2.8		
FLGQQQPFPPQ	<u>1801</u>					31		
LGQQQPFPPQ	<u>1802</u>					151		
QFLGQQQPFPP	<u>1803</u>					2.3		
QFLGQQQPF	<u>1804</u>					5.3		
IRNLALQTLPAMCNVY	<u>1805</u>					1.9		
NLALQTLPAMCNVY	<u>1806</u>					27		
LALQTLPAMCNVY	<u>1807</u>					153		
IRNLALQTLPAM	<u>1808</u>					2.0		
IRNLALQTLP	<u>1809</u>					3.0		

HLA-DR SUPERTYPE								
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
EGDAFELTVSCQGGLP	<u>1810</u>							
K								
ESTGMTPEKVPVSEVM			>17500			>64444.4		
GT	<u>1811</u>					4		
FPTIPLSRLFDNASL	<u>1812</u>	30675	7495	1390	2585	194	5799	
RLFDNASLRAHRLHQ	<u>1813</u>	12461	84	85	11411	3210	557	
LRAHRLHQLAFDITYQ	<u>1814</u>	3208	7590	90	19811	2.0	4471	
QLAFDITYQEFEEAYI	<u>1815</u>	>15384.62	15167	23166	595	11495	>38610.04	
QEFEEAYIPKEQKYS		12821	>15837.1	>15582.1	>54554.47	>41134.7	5418	
	<u>1816</u>			9		5		
IPKEQKYSFLQNPQT	<u>1817</u>	>15384.62	13695	16207	30572	55587	13118	
SFLQNPQTSLCFSES	<u>1818</u>	>15384.62	190	6513	93809	21651	>9647.76	
TSLCFSESIPTPSNR	<u>1819</u>	>15384.62	99	1944	3920	1883	>38610.04	
REETQQKSNELELLRI		>15384.62	15709	9736	>270270.27	52	25133	
	<u>1820</u>							
SNLELLRISLLLIQS	<u>1821</u>	23669	196	59	>91901.83	147	50110	
ISLLLIQSWLEPVQF	<u>1822</u>	2675	120	60	6765	2.5	>9960.16	
SWLEPVQFLRSVFAN	<u>1823</u>	2715	4322	136	>270270.27	291	4815	
FLRSVFANSLVYGAS	<u>1824</u>	973	5.6	13	157978	814	141	
NSLVYGASDSNVYDL	<u>1825</u>	>15384.62	14038	3640	11769	1792	>13046.31	
SDSNVYDLLKDLEEG		>15384.62	>17857.14	>30536.9	219298	>137767.	>13046.31	
	<u>1826</u>			1		22		
GIQTLMGRLEDGSPR	<u>1827</u>	4474	10433	1348	186220	2110	18006	
RLEDGSPRTGQIFKQ	<u>1828</u>	7896	>17857.14	9106	18119	296	12580	
RTGQIFKQTYSKFDT	<u>1829</u>	6961	66	155	14736	201	64	
QTYSKFDTNSHNDDA		>15384.62	>17857.14	25883	38715	>137767.	5787	
	<u>1830</u>					22		
TNSHNDDALLKNYGL		>15384.62	5169	133	130378	>137767.	>13046.31	
	<u>1831</u>					22		
ALLKNYGLLYCFRKD	<u>1832</u>	>15384.62	10	17	2309	1230	462	
DMDKVETFLRIVQCR	<u>1833</u>	885	1232	201	>27322.4	826	7447	
FLRIVQCRSVEGSCGF	<u>1834</u>	2708	1017	839	>27322.4	1078	7102	
FPTIPLSRLFDNAML	<u>1835</u>	46404	9313	2770	121212	216	11521	
RLFDNAMLRAHRLHQ	<u>1836</u>	267	738	18	>270270.27	1628	58	
QLAFDITYQEFEQNPQ		>15384.62	19718	>86666.6	738	>32842.5	>9510.22	
	<u>1837</u>			7		8		
SFLQNPQTSLCCFRK	<u>1838</u>	3801	128	103	>270270.27	8500	3739	
SNLELLRICLLLIQS	<u>1839</u>	>15384.62	773	90	17024	164	>11771.33	
ICLLLIQSWLEPVQF	<u>1840</u>	>15384.62	954	1771	187970	49	>9510.22	
NSLVYGASDSNIYDL	<u>1841</u>	>15384.62	10854	971	31616	3287	>9510.22	
SDSNYDLLKDLEEG		>15384.62	>16203.7	>86666.6	>18726.59	24259	>9510.22	
	<u>1842</u>			7				
DKVETFLRIVQCCGF	<u>1843</u>	1023	1034	383	6278	184	6350	
SFLQNPQTSLTFSES	<u>1844</u>	>15384.62	121	1511	864	17824	12365	
TSLTFSESIPTPSNR	<u>1845</u>	22152	16	176	>95238.1	3476	>1335.38	
ALLKNYGLLYTFRKD	<u>1846</u>	1737	0.89	6.5	50	1335	29	
LLYTFRKDMDKVETF	<u>1847</u>	7905	>14522.82	886	941	12493	154	
DMDKVETFLRIVQTR		206	3381	>86666.6	13712	190	1263	
	<u>1848</u>			7				
FLRIVQTRSVEGSTGF	<u>1849</u>	143	1.5	9.8	27345	21	116	
HLDMLRHLYQGCQVV	<u>1850</u>	2076	2879	359	107066	163	7087	
RLRIVRGTLFEDNYAL	<u>1851</u>	2072	5.2	31	1198	120	46	
GVGSPYVSRLLGICL	<u>1852</u>	696	955	46	148588	316	14197	
TLERPKTLPKGKNGV	<u>1853</u>	>52631.58	835	23264	>263157.89	25739	11337	

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Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
KIFGSLAFLPESFDGDP		>52631.58	1073	2264	43745	10020	8008	
A	<u>1854</u>							
ELVSEFSRMARDPQ	<u>1855</u>	4573	>71428.57	7891	15838	970	4055	
GEALSTLVNLRLKVG	<u>1856</u>	79	29	269		1023	46	
AYVLLSEKKISSIQS	<u>1857</u>	51	816	489		902	4517	
VASLLTTAEVVVTEI	<u>1858</u>	>18674.14	>10294.12	>50837.9		>26435.7	>119047.6	
KCEFQDAYVILLSEKK	<u>1859</u>	1078	>10294.12	>47643.9		>19594.5	20	
ALSTLVNLRLKVGLQ	<u>1860</u>	9.1	4.6	191		17	3.9	
MSYNLLGFLQRSSNC	<u>1861</u>	3628	1190	89	>42194.09	6503	710	
LGFLQRSSNCQCQKL	<u>1862</u>	6025	112	1397	>42194.09	1167	649	
RSSNCQCQKLLWQLN	<u>1863</u>	>408163.27	6153	802	3519	21	6981	
QCQKLLWQLNGRLEY	<u>1864</u>	1644	227	175	8709	209	924	
LWQLNGRLEYCLKDR	<u>1865</u>	4215	808	893	29028	15576	3241	
GRLEYCLKDRRNFDI	<u>1866</u>	1707	1240	940	5213	15870	64725	
RNFDIPEIKQLQQF	<u>1867</u>	7326	>15418.5	2036	23832	311	6854	
PEEIKQLQQFQKEDA	<u>1868</u>	1953	13325	1873	>26315.79	215	675	
QLQQFQKEDAAVTIY	<u>1869</u>	>408163.27	68	1724	348	1338	4270	
QKEDAAVTIYEMLQN	<u>1870</u>	>408163.27	7315	1146	>42194.09	15173	>10482.18	
AVTIYEMLQNIFAIF	<u>1871</u>	29718	109	262	2828	1118	14047	
EMLQNIFAIFRQDSS	<u>1872</u>	36832	61	1718	726	164	3187	
IFAIQRDSSSTGWN	<u>1873</u>	4558	775	204	2181	30	109290	
RQDSSSTGWNETIVE	<u>1874</u>	>42553.19	848	>189583.33	9172	1497	8650	
STGWNETIVENLLAN	<u>1875</u>	20576	105	897	>26315.79	166	5822	
ETIVENLLANVYHQR	<u>1876</u>	>42553.19	8.5	1603	>42194.09	2503	18559	
NLLANVYHQRNHLKT	<u>1877</u>	8258	61	20	>123456.79	3071	65	
VYHQRNHLKTVLEEK	<u>1878</u>	22002	1267	1662	>123456.79	9585	4.7	
LEKEDFTRGKRMSL	<u>1879</u>	698	25362	14118	6267	16057	4903	
FTRGKRMSLHLKRY	<u>1880</u>	81	10245	118	18836	2027	84	
RMSSLHLKRYYGRIL	<u>1881</u>	1035	2532	1.3	>26178.01	2255	491	
HLKRYYGRILHYLKA	<u>1882</u>	2721	868	0.69	6608	22	2.3	
YGRILHYLKAKEDSH	<u>1883</u>	812	2783	16	454545	140	39	
HYLKAKEDSHCAWTI	<u>1884</u>	>60606.06	11571	627	301205	7501	2632	
KEDSHCAWTIVRVEI	<u>1885</u>	9320	506	1397	>1754385.9	7.9	4056	
CAWTIVRVEILRNFY	<u>1886</u>	4167	147	196	10300	152	4143	
VRVEILRNFYVINRL	<u>1887</u>	504	5.8	1.04	80386	187	485	
RNFYVINRLTGILRN	<u>1888</u>	55	9.4	18	689	1249	5.6	
MSYNLLGFLQRSSNT	<u>1889</u>	3069	1334	6.8	51787	4660	9.0	
LGFLQRSSNTQTQKL	<u>1890</u>	26247	21	2331	>1754385.9	1041	339	
RSSNTQTQKLLWQLN	<u>1891</u>	>42553.19	169	2740	751	26	8545	
QTQKLLWQLNGRLEY	<u>1892</u>	20654	121	20	6582	88	417	
LWQLNGRLEYTLKDR	<u>1893</u>	6521	2447	853	4402	14310	6004	
GRLEYTLKDRRNFDI	<u>1894</u>	4998	1468	168	9901	21427	796	
HYLKAKEDSHTAWTI	<u>1895</u>	>60606.06	2264	529	35829	11750	19617	
KEDSHTAWTIVRVEI	<u>1896</u>	7443	3046	1992	56205	18	575	
TAWTIVRVEILRNFY	<u>1897</u>	5052	72	242	14419	26	518	
LGFLQRSSNCQSQKL	<u>1898</u>	604	131	541	>1754385.9	124	508	

HLA-DR SUPERTYPE								
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
					6			
RSSNCQSQKLLWQLN	<u>1899</u>	>60606.06	1960	2962	68823	27	4077	
QSQKLLWQLNGRLEY	<u>1900</u>	>60606.06	155	108	5609	166	402	
GIVEQCCTSICSLYQ	<u>1901</u>	7940	239	1280	14353	4245	>37593.98	
TSICSLYQLENYCN	<u>1902</u>	>10526.32	>15021.46	837	8048	13496	>40322.58	
GILEQCCTSICSLYQ	<u>1903</u>	>10526.32	858	1097	>18726.59	5871	19231	
GIVEQTTTSITSLYQ	<u>1904</u>	>10526.32	14	849	>95238.1	2303	>37593.98	
EQTTSITSLYQLEN	<u>1905</u>	>10526.32	16949	1078	>18726.59	29614	48505	
TSICSLYQLENYCG	<u>1906</u>	>10526.32	10346	173	>95238.1	1645	>40322.58	
TSITSLYQLENYTN	<u>1907</u>	1095	>17073.17	99	>95238.1	3245	6048	
TSITSLYQLENYTG	<u>1908</u>	1014	>17073.17	182	92336	1658	16073	
GIVEQCCCGSHLVEA	<u>1909</u>	>10526.32	15347	237	14184	11017	>43290.04	
SLYQLENYCCGERGF	<u>1910</u>	>1111111.11	>15909.09	151	92336	30978	>43290.04	
CCTSICSLYQLENYCC	<u>1911</u>	>1111111.11	7096	877	>18726.59	1582	>40650.41	
GSHLVEALYLVCNN	<u>1912</u>	>1111111.11	3259	11191	>18726.59	14065	>46403.71	
CCGSHLVEALYLVC	<u>1913</u>	>10526.32	6027	12986	>18726.59	11357	>43290.04	
FDVNHLCGSHLVEAL	<u>1914</u>	>1111111.11	10595	1195	>95238.1	3153	47170	
QHLGSHLVEALYLV	<u>1915</u>	>10526.32	7624	103	14819	1480	32049	
GSHLVEALYLVGER	<u>1916</u>	>10526.32	8030	1350	>18726.59	372	29283	
VEALYLVGERGFFY	<u>1917</u>	3563	4403	181	4443	30	25543	
YLVCGERGFFYTPKT	<u>1918</u>	>10526.32	9272	10655	92764	34450	95238	
FDVNHLCGSDLVEAL	<u>1919</u>	>1111111.11	20248	9679	10031	24511	>43290.04	
FDVNHLTGSHLVEAL	<u>1920</u>	>10526.32	12413	799	94518	4084	>43290.04	
QHLTGSHLVEALYLV	<u>1921</u>	>10526.32	6862	184	4027	939	23716	
GSHLVEALYLVTER	<u>1922</u>	>10526.32	12185	1429	18215	225	11398	
VEALYLVGERGSFY	<u>1923</u>	>10526.32	4288	1240	>95238.1	129	804	
VEALYLVGERGFLY	<u>1924</u>	55402	1871	149	843	19	5149	
VEALYLVTERGFFY	<u>1925</u>	4860	1076	116	17156	13	78	
YLVCGERGFLYTPKT	<u>1926</u>	>1111111.11	2120	>25633.8	>95238.1	33114	971	
YLVCGERGFFYTDKT	<u>1927</u>	>60606.06	1014	>25633.8	616	48099	>28449.5	
YLVCGERGFFYTKPT	<u>1928</u>	>60606.06	3467	>25633.8	12805	40379	>28449.5	
YLVTERGFFYTPKT	<u>1929</u>	7625	2100	>25633.8	13737	20721	>28449.5	
YLVTERGFFYTDKT	<u>1930</u>	16849	17353	>25633.8	359	30824	>28449.5	
YLVTERGFFYTKPT	<u>1931</u>	9341	17869	>21016.1	9573	27915	11926	
VCGERGFFYTPKTRR	<u>1932</u>	3817	34669	>25633.8	17416	>30999.4	92	
VTGERGFFYTPKTRR	<u>1933</u>	10116	25362	2824	243902	>29820.0	540	
MWDLVLSIALSVGCT	<u>1934</u>	81096	108	11375	15205	158	70711	
DLVLSIALSVGCTGA	<u>1935</u>	>200000	98	18200	>14918.69	459	>100000	
HPQWVLTAHCLKKN	<u>1936</u>	981	483	1219	8114	1106	11	
QWVLTAHCLKKN SQ	<u>1937</u>	14213	>35000	>45500	>14918.69	14395	382	
GQRVPVSHSFPHPLY	<u>1938</u>	>200000	703	3960	>14918.69	9860	>200000	
RVPVSHSFPHPLYNM	<u>1939</u>	>200000	377	5518	>14918.69	9213	11650	
PHPLYNMSLLKHQSL	<u>1940</u>	6455	3307	3873	>14918.69	49	1901	
HPLYNMSLLKHQSLR	<u>1941</u>	248	546	472	>14918.69	8.4	219	
NMSLLKHQSLRPDED	<u>1942</u>	25820	>35000	>30333.3	>14918.69	105	>100000	

HLA-DR SUPERTYPE								
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
SHDLMLLRLSEPAKI	<u>1943</u>	5267	1.8	365	5361	10	2031	
HDLMLLRLSEPAKIT	<u>1944</u>	1147	0.83	115	488	12	211	
PEEFLRPRSLQCVSL	<u>1945</u>	10675	11667	3193	>14413.38	117	57537	
PRSLQCVSLHLLSND	<u>1946</u>	11128	3731	1597	11650	544	46416	
NGVLQGITSWGPEPC	<u>1947</u>	32444	>17500	835	>14413.38	5761	>100000	
KPAVYTKVVHYRKWI	<u>1948</u>	327	1947	401	7186	4581	23	
LHLLSNDMCAAYSE	<u>1949</u>	26012	1876	>2367.33	1308	324	28817	
VGNWQYFFPVIFSKA	<u>1950</u>							
ESEFQAALSRKVAKL	<u>1951</u>							
IGHLYIFATCLGLSYDG L	<u>1952</u>							
VGNWQYFFPVIFSKAS								
DSLQLVFGIELMEVD	<u>1953</u>							
PAYEKLSAEQSPPPY	<u>1954</u>							
RNGYRALMDKSLHVG								
TQCALTRR	<u>1955</u>							
FFKNIVTFFKNIVT	<u>1956</u>							
YKSAHKGFGKVDAQG		2000					1333	2065
TLSKI	<u>1957</u>							
VDAQGTLSKIFKLGGGR		18			769		6667	1152
DSRS	<u>1958</u>							
AC-		200000					200000	4561
ASQKRPSQRHGSKYLA								
TAST	<u>1959</u>							
ENPVVHFFKNIVTPR	<u>1960</u>			5.2			463	
ENPVVAFFKNIVTPR	<u>1961</u>			2.8			302	
ENPVVHAFKNIVTPR	<u>1962</u>			4.1			910	
ENPVVHFFANIVTPR	<u>1963</u>			2.9			6235	
ENPVVHFFKNIVTPA	<u>1964</u>			2.5			3333	
NPVVHFFKNIVT	<u>1965</u>			23			10000	
HFFKNIVTPRTPPY	<u>1966</u>			460			377	
NPVVHFFKNIVTPR	<u>1967</u>			3.7			1890	
LPVPGVLLKEFTVSGNI		216	52	84		349	1840	
LTl	<u>1968</u>							
WITQCFLPVFLAQPPSG		13208	23649	726		688	286	
QRR	<u>1969</u>							
DHRQLQLSISSCLQQLS		>98522.17	69	67		532	63772	
LLM	<u>1970</u>							
YLAMPFATPMEAEAR		3754	2813	865		1965	641	
RSLA	<u>1971</u>							
AAPLLLARAASLSLG	<u>1972</u>	100	3.2	35	10470	79	79	
APLLLARAASLSLGF	<u>1973</u>	322	12	91	13359	59	114	
PLLLARAASLSLGFL	<u>1974</u>	1255	12	118	>9742.79	52	151	
SLSLGFLFLFFWLD	<u>1975</u>	100000	639	11375	3710	>10955.8	66667	
LLFFWLD RSVLAKEL	<u>1976</u>	154	24	34	86	7.5	134	
DRSVLAKELKFVTLV	<u>1977</u>	20966	4410	1359	>14413.38	53	2217	
AKELKFVTLVFRHGD	<u>1978</u>	12309	824	1529	8563	51	24	
RSPIDTFPTDPIKES	<u>1979</u>	>200000	>35000	2373	>14413.38	469	28571	
FGQLTQLGMEQHYEL	<u>1980</u>	27217	>35000	>22750	>14413.38	543	100000	
DRTLMSAMTNLAALF	<u>1981</u>	2367	114	871	3927	57	26138	
MSAMTNLAALFPPEG	<u>1982</u>	>200000	249	12384	7158	1072	63246	
MTNLAALFPPEGVSI	<u>1983</u>	141421	1310	10370	>8829.24	4606	141421	
PEGVSIWNPIILLWQP	<u>1984</u>	30861	444	7.2	4624	107	22222	
GVSIWNPIILLWQPIP	<u>1985</u>	10287	207	5.0	4428	492	523	

HLA-DR SUPERTYPE								
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
WNPILLWQPIPVHTV	<u>1986</u>	19640	2259	14	>8829.24	81	100000	
NPILLWQPIPVHTVP	<u>1987</u>	599	250	4.6	>8829.24	67	25000	
PILLWQPIPVHTVPL	<u>1988</u>	4041	567	6.9	>8829.24	106	41491	
ILLWQPIPVHTVPLS	<u>1989</u>	2343	1111	65	>8829.24	712	28768	
WQPIPVHTVPLSEDQ	<u>1990</u>	>66666.67	2692	>45500	>8829.24	1228	>100000	
LSGLHGQDLFGIWSK	<u>1991</u>	30151	>35000	32173	>8829.24	135	81650	
YDPLYCESVHNFTLP	<u>1992</u>	30151	>35000	2136	>8829.24	6901	28768	
LPSWATEDMTKRLRE	<u>1993</u>	>66666.67	>35000	>45500	5973	>11134.5 7	343	
LRELSESLLSLYGI	<u>1994</u>	6958	3218	235	>14956.63	544	5185	
LSESLLSLYGIHKQ	<u>1995</u>	1657	1253	45	>13046.31	79	7.3	
LSLLSLYGIHKQKEK	<u>1996</u>	742	>35000	58	>14956.63	772	3.4	
KSRLQGGLVNEILN	<u>1997</u>	>66666.67	318	>30333.3 3	>14956.63	713	>100000	
GGVLVNEILNHMKRA	<u>1998</u>	255	49	576	8124	5.8	8.7	
IPSYKKLIMYSAHDT	<u>1999</u>	53	2122	17	9982	12	191	
YKKLIMYSAHDTTVS	<u>2000</u>	208	37	15	13224	5.8	5482	
LIMYSAHDTTVSGLQ	<u>2001</u>	>66666.67	1752	184	6828	4381	>100000	
DTTVSGLQMALDVYN	<u>2002</u>	>50000	3500	1042	10843	961	>200000	
ALDVYNGLLPPYASC	<u>2003</u>	182	>35000	1091	>14956.63	>10090.4 7	115470	
LDVYNGLLPPYASCH	<u>2004</u>	194	>35000	3035	>14956.63	>10918.6 7	25820	
YNGLLPPYASCHLTE	<u>2005</u>	5300	11667	252	>14956.63	>10918.6 7	100000	
FAELVGVPVQDWST	<u>2006</u>	>50000	>35000	>45500	>14956.63	983	>200000	
TVPLSEDQLLYLPFR	<u>2007</u>	26455	5300	>2367.33	4323	872	27221	
LTELYFEKG EYFVEM	<u>2008</u>	>18903.59	3157	>2367.33	124	601	6655	
GPVIPQDWSTECMTT	<u>2009</u>				20295	961		
QAHSRLRVCHCLGKWL	<u>2010</u>	2857					2500	
GHPDK	<u>2011</u>	40000		277	37450	505	400	
WTTCSIAFPSKTSASIG	<u>2012</u>	30151		>9100	>500000	17951	9759	
SL	<u>2013</u>	17		239	70014	1218	18	
QKGRGYRGQHAHSLE	<u>2014</u>	33333			117851	193333		
RVCH	<u>2015</u>			45			256	
AATYNFAVLKLMGRGT	<u>2016</u>			92			20000	
KF	<u>2017</u>	6860	642	97	6031	3506	31	
VATGLCFFGVALFCGC	<u>2018</u>	2196	420	147	13676	42	104	
GHEA	<u>2019</u>	1779	2339	552	>10729.61	88	147	
FLYGALLAEGFYTTG	<u>2020</u>	135	32	11259	>12116.81	7562	84	
AVRQ	<u>2021</u>	>50000	5456	12888	>12116.81	62	100000	
SAVPVYIYFNTWTTCS	<u>2022</u>	263	2427	66	>10729.61	6.2	1062	
IAF	<u>2023</u>	785	1170	6500	1324	5518	40	
TLSVTWIGAAPLILS	<u>2024</u>	2169	2062	13565	7342	3802	35	
SVTWIGAAPLILSRI	<u>2025</u>	93	75	88	4752	8.7	3630	
VTWIGAAPLILSRIV	<u>2026</u>	96	96	106	13045	4411	16116	
SQPWQVLVASRGRAV	<u>2027</u>	344	543	426	>12116.81	10696	100000	
GRAVCGGLVHPQWV	<u>2028</u>	103	146	2172	1071	416	128	
GVLVHPQWVLTAHHC								
HPQWVLTAAH CIRNK								
QWVLTAAH CIRNKSV								
AHCIRNKSVILLGRH								
SVILLGRHSLFHPED								
VILLGRHSLFHPEDT								
GQVFQVSHSFHPPLY								

HLA-DR SUPERTYPE								
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
VFQVSHSFPHPLYDM	<u>2029</u>	881	83	2396	23433	>12491.9	897	
PHPLYDMSLLKNRFL	<u>2030</u>	>50000	11667	712	>13533.63	7486	3104	
SHDLMLLRLSEPAEL	<u>2031</u>	4471	5.8	1099	13577	12	100000	
HDLMLLLRLSEPAELT	<u>2032</u>	2141	2.3	662	5305	45	10541	
TDVAVKMDLPTQEPA	<u>2033</u>	>50000	>35000	>45500	>13533.63	747	>200000	
LHVISNDVCAQVHPQ	<u>2034</u>	>50000	239	22750	1887	1087	>200000	
CAQVHPQKVTKFMLC	<u>2035</u>	18490	2192	809	>13533.63	604	1229	
GGPLVCNGVLQGITS	<u>2036</u>	1828	36	30333	>6567.28	815	13417	
GPLVCNGVLQGITSW	<u>2037</u>	915	49	6310	11615	646	6537	
NGVLQGITSWGSEPC	<u>2038</u>	9724	775	258	8038	4487	11619	
RPSLYTKVVHYRKWI	<u>2039</u>	350	4183	717	2982	4897	13	
HSLFHPEDTGQVFQV	<u>2040</u>				553	11503		
PRWLCAGALVLAGGF	<u>2041</u>	>40000	20207	15167	13150	883	40825	
LGFLFGWFIKSSNEA	<u>2042</u>	7303	10104	355	681	9285	461	
LDELKAENIKKFLYN	<u>2043</u>	324	597	414	548	788	150	
IKKFLYNFTQIPHLA	<u>2044</u>	137	27	305	477	96	658	
KFLYNFTQIPHLAGT	<u>2045</u>	91	221	227	10212	256	1600	
WKEFGLDSVELAHYD	<u>2046</u>	4935	8413	22750	829	5925	89443	
LAHYDVLLSYPNKTH	<u>2047</u>	380	268	82	1406	589	172	
GNEIFNTSLFEPPPP	<u>2048</u>	>40000	2804	>91000	>13164.82	835	>200000	
GKVFRGNKVKNQAQLA	<u>2049</u>	894	46	3373	7591	7884	1385	
GNKVKNQLAGAKGV	<u>2050</u>	>66666.67	>35000	>45500	>12462.61	1065	1218	
EYAYRRGIAEAVGLP	<u>2051</u>	2590	5217	>45500	8773	6325	1204	
AEAVGLPSIPVHPIG	<u>2052</u>	>66666.67	5456	56	>11848.34	12394	69336	
AVGLPSIPVHPIGYY	<u>2053</u>	33333	1191	518	>11848.34	5387	38517	
IGYYDAQKLEKMG	<u>2054</u>	>28571.43	5729	1978	17305	13588	506	
TGNFSTQKVKMHIHS	<u>2055</u>	11856	6187	3745	>11848.34	508	1927	
TRIYNVIGTLRGAVE	<u>2056</u>	45	1460	1605	17550	447	32	
ERGVAYINADSSIEG	<u>2057</u>	>50000	3689	30333	6846	87	200000	
GVAYINADSSIEGNY	<u>2058</u>	>40000	497	7610	1420	477	66667	
DSSIEGNYTLRDCT	<u>2059</u>	>50000	7.6	1202	576	1262	16824	
NYTLRDCTPLMYSL	<u>2060</u>	7116	9.0	5056	25	404	66667	
CTPLMYSLVHNLTK	<u>2061</u>	590	260	426	18348	58	36	
DFFVFFQRLGIASGR	<u>2062</u>	128	10069	10249	30745	4.2	3559	
EVFFQRLGIASGRAR	<u>2063</u>	31	17500	4556	>15037.59	51	7.9	
TNKFSGYPLYHSVYE	<u>2064</u>	33333	>35000	489	>21853.15	12466	2942	
YDPMFKYHLTVAQVR	<u>2065</u>	252	1014	1348	8137	553	62	
DPMFKYHLTVAQVRG	<u>2066</u>	69	699	230	7297	467	11	
MFKYHLTVAQVRGGM	<u>2067</u>	147	1615	1198	3648	1062	5.8	
KYHLTVAQVRGGMVF	<u>2068</u>	859	193	1222	>21853.15	3446	86	
VAQVRGGMVFEANS	<u>2069</u>	>50000	2802	117	>21853.15	100	64366	
RGGMVFEANSIVLP	<u>2070</u>	>50000	4.4	94	132	411	413	
GMVFEANSIVLPFD	<u>2071</u>	>50000	12	83	234	4154	903	
VFELANSIVLPFDCR	<u>2072</u>	11765	24	477	128	1215	10815	
ADKIYSISMKHPQEM	<u>2073</u>	169	4957	8273	>21853.15	3550	26726	
IYSISMKHPQEMKTY	<u>2074</u>	213	>35000	5025	>21853.15	5356	2588	

HLA-DR SUPERTYPE								
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
PQEMKTYSVSFDSL	<u>2075</u>	>50000	24749	919	14564	579	100000	
TYSVSFDSLFSVKN	<u>2076</u>	5981	5888	3223	8547	10461	61	
VLRMMNDQLMFLERA	<u>2077</u>	2353	130	127	98	88	85	
LRMMNDQLMFLERAF	<u>2078</u>	1833	1314	1411	1570	50	758	
RHVIYAPSSHKNKYAG	<u>2079</u>	13363	8750	1291	>62814.07	5293	88	
RQIYVAAFTVQAAAE	<u>2080</u>	35	524	166	6808	47	143	
QIYVAAFTVQAAAET	<u>2081</u>	34	344	252	1324	50	216	
VAAFTVQAAAETLSE	<u>2082</u>	2126	446	18200	2116	464	378	
YISINEDGNEIFNT	<u>2083</u>	>18903.59	346	2713	30	3705	72993	
ISIINEDGNEIFNTS	<u>2084</u>	>18903.59	343	3006	35	6394	>37807.18	
EDFFKLERDMKINCS	<u>2085</u>	10433	3188	>3490.6	4036	7886	3494	
FFKLERDMKINCSGK	<u>2086</u>	9687	382	>3490.6	4918	98	3796	
GVILYSDPADYFAPG	<u>2087</u>	>18903.59	39	965	8.8	64	14168	
GAAVVHEIVRSFGTL	<u>2088</u>				788	89		
NSRLQERGVAYINA	<u>2089</u>	12812	327	1229	3366	699	3473	
VAYINADSSIEGNYT	<u>2090</u>	>18903.59	2147	>3490.6	471	841	>37807.18	
DQLMFLERAFIDPLG	<u>2091</u>				17115	6.6		
KSNFLNCYVSGFHPSD	<u>2092</u>	5000					2857	
AC- NPDAENWNSQFEILED AA	<u>2093</u>	>33333.33	>10000	>10000	1000		50000	
EYLILSARDVLAVVS	<u>2094</u>	6860		2340		2527	4154	
YKTIAYDEEARR	<u>2095</u>	200000		>91000	>50000		200000	
GEALSTLVVNKIRGT	<u>2096</u>	977	55	2314		1514	108	
PYILLVSSKYSTVKD	<u>2097</u>	112	7.2	22		107	32	
EAVLEDPYILLVSSK	<u>2098</u>	4376	>10294.12	>50837.9 9		>26435.7 3	357	
IAGLFLTTEAVVADK	<u>2099</u>	867	>10294.12	>50837.9 9		>26435.7 3	606	
ALSTLVVNKIRGTFK	<u>2100</u>	32	7.6	160		214	38	
MKHILYISFYFILVN	<u>2101</u>	2082					>9523.81	
KSLLSTNLPGYGRTNL	<u>2102</u>							
HFFLLLYILFLVKM	<u>2103</u>		84	21473		1064	10083	
LFLLYILFLVKMNAL	<u>2104</u>		129	30829		1290	32446	
ILFLVKMNALRRLPV	<u>2105</u>		0.13	1.4		7.6	14	
MNALRRLPVICSLV	<u>2106</u>		15	36		5.7	2557	
SAFLESQSMNKIGDD	<u>2107</u>		52	18689		302	243	
LKELIKVGLPSFENL	<u>2108</u>		147	361		110	41322	
FENLVAENVKPPKVD	<u>2109</u>		3029	>50837.9 9		9297	62661	
PATYGHVPVLTSLF	<u>2110</u>		0.83	2557		118	52	
YGIIVPVLTSLFNKV	<u>2111</u>		0.30	223		97	80	
LLKIWKNYMKIMNHL	<u>2112</u>		3.7	6.8		12	35	
MTLYQIQVMKRNQKQ	<u>2113</u>		323	2429		82	22	
QKQVQMMIMIKFMGV	<u>2114</u>		17	363		5.3	915	
MIMIKFMGVYIMII	<u>2115</u>		102	23611		145	12310	
GVIYIMIISKMMMRK	<u>2116</u>		38	173		157	46	
LYYLFNQHIKKELYH	<u>2117</u>		327	2861		1089	606	
HFNMLKNKMQSSFFM	<u>2118</u>		54	616		934	60	

HLA-DR SUPERTYPE								
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
LDIYQKLYIKQEEQK	<u>2119</u>		4346	47		70	6958	
QKKYIYNLIMNTQNK	<u>2120</u>		53	844		87	245	
YEALIKLLPFSKRIR	<u>2121</u>		230	36		15	11	
ENEYATGAVRPFQAA	<u>2122</u>		9302	3007		10026	>10303.97	
NYELSKKAVIFTPIY	<u>2123</u>		410	537		136	10581	
QKILIKIPVTKNIIT	<u>2124</u>		332	3614		953	297	
KCLVISQVSNDSYK	<u>2125</u>		236	403		81	>42553.19	
SKIMKLPKLPISNGK	<u>2126</u>		6460	3570		6739	>10303.97	
FIHFFTWTGTMFVPKY	<u>2127</u>		328	2375		387	9608	
LCNFKKNIIALLIIP	<u>2128</u>		16	29302		99	>42553.19	
KKNIIALLIIPPKIH	<u>2129</u>		15	32		8.2	143	
ALLIIPPKIHISIEL	<u>2130</u>		162	1823		10	7135	
SMEYKKDFLITARKP	<u>2131</u>		3818	4610		10448	442	
KSKFNILSSPLFNNF	<u>2132</u>		25	5.9		135	32	
FKKLNHVLFLQMMN	<u>2133</u>		20	29		14	59	
KNHVLFLQMMNVNLQ	<u>2134</u>		36	224		22	>7212.41	
VLFLQMMNVNLQKQL	<u>2135</u>		8.6	8200		12	>7212.41	
NVNLQKQLLTNHLIN	<u>2136</u>		28	4448		354	>7212.41	
QKQLLTNHLINTPKI	<u>2137</u>		1.6	514		904	6595	
NHLINTPKIMPHII	<u>2138</u>		32	560		1632	8882	
YILLKKILSSRFNQM	<u>2139</u>		1.01	26		340	83	
FNQMIFVSSIFISFY	<u>2140</u>		33	3903		1291	>12484.39	
KVSCKGSGYTFTAYQM		>200000						
H	<u>2141</u>							
IAKVPPGNITAEGDK		200000			>20000		200000	
WLD	<u>2142</u>							
TAEYGDKWLDKSTW		200000			>20000		10000	
YGKPT	<u>2143</u>							
AKSTWYGKPTGAGPKD		200000			>20000		10000	
NGGA	<u>2144</u>							
GAGPKDNGGACGYKD		200000			>20000		200000	
VDKAP	<u>2145</u>							
FNGMTGCGNTPIFKDG		200000			>20000		200000	
RGCG	<u>2146</u>							
PIFKDGRGCGSCFEIKC		200000			>20000		200000	
TKP	<u>2147</u>							
SCFEIKCTKPESCSGEA		200000			>20000		200000	
VTV	<u>2148</u>							
AFGSMAKKGEEQNVR		1818			>33333.33		200000	
AGEL	<u>2149</u>							
TPDKLTGPFTVRYTTEG		200000			>25000		200000	
GTK	<u>2150</u>							
VRYTTEGGTKSEVEDVI		200000			>25000		200000	
PEG	<u>2151</u>							
TCVLGKLSQELHKLQ	<u>2152</u>	1398	>12589.93	2009	>263157.89	163	3986	
KLSQELHKLQTYPR	<u>2153</u>	2375	>12589.93	287	>263157.89	870	37	
LHKLQTYPRNTGSG	<u>2154</u>	6091	>12589.93	157	>263157.89	22948	40	
KLQTYPRNTGSGTP	<u>2155</u>	8210	987	520	>263157.89	>104693.14	>14044.94	
CCVLGKLSQELHKLQ	<u>2156</u>	5243	>12589.93	570	>263157.89	346	5158	
CSNLSTCVLGKLSQE	<u>2157</u>	5263	7907	4538	>263157.89	11756	5709	
TSNLSTTVLGKLSQE	<u>2158</u>	534	9333	7697	>263157.89	13210	2529	
TTVLGKLSQELHKLQ	<u>2159</u>	3524	12715	525	>263157.89	241	10618	
DIAAKYKELGY	<u>2160</u>	>10000			>25000		200000	
ALVRQGLAKVA	<u>2161</u>	200000					>10000	

HLA-DR SUPERTYPE								
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
PATLIKAIDGDTVKLMY		>6666.67			2381		3333	
KGQ	<u>2162</u>							
TPETKHPKKGVEKYGP		>6666.67			>25000		>4000	
EASA	<u>2163</u>							
VEKYGPEASAFKKMV		20000			16667		34	
ENAK	<u>2164</u>							
FTKKMVENAKKIEVEF		6667			>25000		1000	
DKGQ	<u>2165</u>							
YIYADGKMOVNEALVRQ		>6666.67			>5555.56		>4000	
GLAK	<u>2166</u>							
HEQHLRKSEAQAQKEK		200000			>5555.56		11	
LNIW	<u>2167</u>							
QAKKEKLNIWSEDNAD		200000			>5555.56		200000	
SGQ	<u>2168</u>							
YFNNFTVSFWLRVPK	<u>2169</u>							
FSYFPSI	<u>2170</u>							
YSFFPSI	<u>2171</u>							
YSYFPSIR	<u>2172</u>	20000					>200000	
DPNANPNVDPNANPNV		>12500		>7583.33		>72500	>2898.55	
NANPNANPNANP(X4)	<u>2173</u>							
QKWAAVVVPS	<u>2174</u>							
TWQLNGEELIQDMELV								
ETRPAG	<u>2175</u>							
PEFLEQRRAAVDTYC	<u>2176</u>	488					200000	
STORKUSP33								
DYSYLQSDPDSFQD	<u>2178</u>	>66666.67	>35000	>45500			>40000	
DFSYLQSDPDSFQD	<u>2179</u>		>35000	>91000			>40000	
QNILFSNAPLGPQFP	<u>2180</u>							
QNILLSNAPLVPQFP	<u>2181</u>							
DYSYLQSDPDSFQD	<u>2182</u>							
KYVKQNTLKLAT	<u>2183</u>							
P(X)KQNTLKLAT	<u>2184</u>							
EEDIEIPIQEEY	<u>2185</u>	>20576.13					46083	
HQAISPTLNSPAIF	<u>2186</u>	33686	1036	8106	>83333.33	130	>200000	
YTDVFSLDPTFTIETT	<u>2187</u>							
YAGIRRDGLLLRLVD	<u>2188</u>							
LFFYRKSVWSKLQSI	<u>2189</u>	12	121	20	5915	1933	18	
RPIVNMDYVVGARTFR		222	73	43	3324	160	6.6	
REKR	<u>2190</u>							
RPGLLGASVLGLDDI	<u>2191</u>	>93896.71	2056	6000	30212	22038	>88888.89	
LYFVKVDVTGAYDTI	<u>2192</u>	221	79	9753	16	22	4962	
FAGIRRDGLLLRLVD	<u>2193</u>	804	1294	28	553	1670	1355	
AKTFLRTLVRGVPEY	<u>2194</u>	6.3	94	829	546	472	3484	
YGAVVNLRKTVVNF	<u>2195</u>	89	11236	470	51496	302	36	
GTAQVQMPAHGLFPW	<u>2196</u>	17	2819	1.2	769	2361	43	
WAGLLLDTRTLEVQS	<u>2197</u>	20960	92	3468		862	>102040.8	
RTSIRASLTFNRGFK	<u>2198</u>	4807	49	497		79	52	
RVIKNSIRLTL	<u>2199</u>	1740	32	4317		143	8834	
PVIKNSIKLRL	<u>2200</u>	2772	77	2579		198	1039	
ATSTKKLHKEPATLIKA		>6666.67			462		267	
IDG	<u>2201</u>							

TABLE 28

MURINE CLASS I SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
SGPSNTPPEI	<u>2202</u>	10	Adenovirus	E1A		
RNPRFYNL	<u>2203</u>	8	Artificial sequence	Consensus		
QPQRGYENF	<u>2204</u>	9	Artificial sequence	Consensus		A
SEAAAYAKKI	<u>2205</u>	9	Artificial sequence	pool consensus		A
AYAPAKAAI	<u>2206</u>	9	Artificial sequence			Poly
AYAEAKAAI	<u>2207</u>	9	Artificial sequence			Poly
AYANAKAAI	<u>2208</u>	9	Artificial sequence			Poly
AYAGAKAAI	<u>2209</u>	9	Artificial sequence			Poly
AYAVAKAAI	<u>2210</u>	9	Artificial sequence			Poly
AAAAYAAM	<u>2211</u>	8	Artificial sequence			
AAAAYAAAAAM	<u>2212</u>	10	Artificial sequence			
AAAAANAAM	<u>2213</u>	9	Artificial sequence			
AAAAANAAM	<u>2214</u>	11	Artificial sequence			
NAIVFKGL	<u>2215</u>	8	Chicken	Ova	176	
SIINFEKL	<u>2216</u>	8	Chicken	Ova	257	
IFYCPIAI	<u>2217</u>	8	Chicken	Ova	27	
KVVRFDKL	<u>2218</u>	8	Chicken	Ova	55	
VVSFSLASRL	<u>2219</u>	10	Chicken	Ova	96	
SIINFEKL	<u>2220</u>	8	Chicken	Ova	257	
KVVRFDKL	<u>2221</u>	8	Chicken	Ova	55	
SENDRYRL	<u>2222</u>	9	EBV	BZLF1	209	A
SFYRNLLWL	<u>2223</u>	9	Flu	HA	142	
YEANGNLI	<u>2224</u>	8	Flu	HA	259	A
MGLIYNRM	<u>2225</u>	8	Flu	M1	128	
MGYIYNRM	<u>2226</u>	8	Flu	M1	128	
MGIYNRM	<u>2227</u>	8	Flu	M1	128	
MGLIFNRM	<u>2228</u>	8	Flu	M1	128	
MGLIYNRM	<u>2229</u>	8	Flu	M1	128	
RMIQNSLTI	<u>2230</u>	9	Flu	NP	55	
RLIQNFLTI	<u>2231</u>	9	Flu	NP	55	
GMRQNATEI	<u>2232</u>	9	Flu	NP	17	
YMRVNGKWM	<u>2233</u>	9	Flu	NP	97	
FYIQMATEL	<u>2234</u>	9	Flu	NP	39	
FYIQMCTFL	<u>2235</u>	9	Flu	NP	39	
AYERMANIL	<u>2236</u>	9	Flu	NP	218	
AYQRMCNIL	<u>2237</u>	9	Flu	NP	218	
AYERMCTIL	<u>2238</u>	9	Flu	NP	218	
ASNENMETM	<u>2239</u>	9	Flu	NP	366	
TYQRTRALM	<u>2240</u>	9	Flu	NP	147	A
TYQKTRALV	<u>2241</u>	9	Flu	NP	147	A
TYQPTRALV	<u>2242</u>	9	Flu	NP	147	A
TYQFTRALV	<u>2243</u>	9	Flu	NP	147	A
TYQLTRALV	<u>2244</u>	9	Flu	NP	147	A
SDYEGRLI	<u>2245</u>	8	Flu	NP	50	
MITQFESL	<u>2246</u>	8	Flu	NS	31	
RTFSFQLI	<u>2247</u>	8	Flu	NS	114	
FSVIFDRL	<u>2248</u>	8	Flu	NS	134	

MURINE CLASS I SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
RTFSFQLI	<u>2249</u>	8	Flu	NS1	114	
MITQFESL	<u>2250</u>	8	Flu	NS1	31	
FSVIFDRL	<u>2251</u>	8	Flu	NS2	134	
KSSFYRNL	<u>2252</u>	8	FluA	HA	158	
SSLPFQNI	<u>2253</u>	8	FluA	HA	305	
MNIQFTAV	<u>2254</u>	8	FluA	HA	403	
MNYYWTLL	<u>2255</u>	8	FluA	HA	244	
SFYRNLLWL	<u>2256</u>	9	FluA	HA	160	
SSLPFQNI	<u>2257</u>	8	FluA	HA	305	
MNIQFTAV	<u>2258</u>	8	FluA	HA	403	
MNYYWTLL	<u>2259</u>	8	FluA	HA	244	
KSSFYRNL	<u>2260</u>	8	FluA	HA	158	
SIIPSGPL	<u>2261</u>	8	FluA	M1	13	
LSYSAGAL	<u>2262</u>	8	FluA	M1	117	
LSYSAGAL	<u>2263</u>	8	FluA	M1	117	
SSISFCGV	<u>2264</u>	8	FluA	NM	426	
TGICNQNI	<u>2265</u>	9	FluA	NM	46	
ITYKNSTWV	<u>2266</u>	9	FluA	NM	54	
FCGVNSDTV	<u>2267</u>	9	FluA	NM	430	
TGICNQNI	<u>2268</u>	9	FluA	NM	46	
FCGVNSDTV	<u>2269</u>	9	FluA	NM	430	
ITYKNSTWV	<u>2270</u>	9	FluA	NM	54	
SSISFCGV	<u>2271</u>	8	FluA	NM	426	
IGRFYIQM	<u>2272</u>	8	FluA	NP	36	
MMIWHSNL	<u>2273</u>	8	FluA	NP	136	
ASNENMETM	<u>2274</u>	9	FluA	NP	366	
IGRFYIQM	<u>2275</u>	8	FluA	NP	36	
MMIWHSNL	<u>2276</u>	8	FluA	NP	136	
FFYRYGFV	<u>2277</u>	8	FluA	POL1	495	
KMITQRTI	<u>2278</u>	8	FluA	POL1	198	
RSYLIRAL	<u>2279</u>	8	FluA	POL1	215	
RFYRTCKL	<u>2280</u>	8	FluA	POL1	465	
TALANTIEV	<u>2281</u>	9	FluA	POL1	141	
TALANTIEV	<u>2282</u>	9	FluA	POL1	141	
RSYLIRAL	<u>2283</u>	8	FluA	POL1	215	
RFYRTCKL	<u>2284</u>	8	FluA	POL1	465	
VYINTALL	<u>2285</u>	8	FluA	POL2	463	
VYINTALL	<u>2286</u>	8	FluA	POL2	463	
VYIEVLHL	<u>2287</u>	8	FluA	POL3	227	
VYIEVLHL	<u>2288</u>	8	FluA	POL3	227	
WYIPPSLRTL	<u>2289</u>	10	GAD			
MURTAZAKDPEPTIDE		0	GAD65		107	
S						
IYSTVASSL	<u>2291</u>	9	HA		553	
LYEKVKSQL	<u>2292</u>	9	HA		462	
LYQKVKSQL	<u>2293</u>	9	HA		462	
LYEKMKSQL	<u>2294</u>	9	HA		462	
LYEKVFSQL	<u>2295</u>	9	HA		462	
LYQNVGTYV	<u>2296</u>	9	HA		204	

MURINE CLASS I SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
MGLKFRQL	<u>2297</u>	8	HBV	core	122	
VSyvNTNM	<u>2298</u>	8	HBV	core	115	
SYVNTNMGL	<u>2299</u>	9	HBV	core	116	
MGLKFRQL	<u>2300</u>	8	HBV	core	122	
VSyvNTNM	<u>2301</u>	8	HBV	core	115	
SYVNTNMGL	<u>2302</u>	9	HBV	core	116	
WGPSLYSI	<u>2303</u>	8	HBV	env	364	
ASARFSWL	<u>2304</u>	8	HBV	env	329	
WGPSLYSIL	<u>2305</u>	9	HBV	env	364	
TGPCRTCMT	<u>2306</u>	9	HBV	env	281	
WYWGPSLYSI	<u>2307</u>	10	HBV	env	362	
IPQSLDSWWTSL	<u>2308</u>	12	HBV	env	28	
IPQSLDSYWTS�	<u>2309</u>	12	HBV	env	28	A
ASARFSWL	<u>2310</u>	8	HBV	env	329	
WYWGPSLYSI	<u>2311</u>	10	HBV	env	362	
APQSLDSWWTSL	<u>2312</u>	12	HBV	env	28	
IPQALDSWWTSL	<u>2313</u>	12	HBV	env	28	A
IPQSLASWWTSL	<u>2314</u>	12	HBV	env	28	A
IPQSLDAWWTSL	<u>2315</u>	12	HBV	env	28	A
IPQSLDSAWTSL	<u>2316</u>	12	HBV	env	28	A
IPQSLDSWWASL	<u>2317</u>	12	HBV	env	28	A
IPQSLDSWWTAL	<u>2318</u>	12	HBV	env	28	A
EPQSLDSWWTSL	<u>2319</u>	12	HBV	env	28	A
IPESLDSWWTSL	<u>2320</u>	12	HBV	env	28	A
IPQSLDEWWTSL	<u>2321</u>	12	HBV	env	28	A
IPQSLDSWWTEL	<u>2322</u>	12	HBV	env	28	A
RPQSLDSWWTSL	<u>2323</u>	12	HBV	env	28	A
IPRSLDSWWTSL	<u>2324</u>	12	HBV	env	28	A
IPQRLDSWWTSL	<u>2325</u>	12	HBV	env	28	A
IPQSRDSWWTSL	<u>2326</u>	12	HBV	env	28	A
IPQSLRSWWTSL	<u>2327</u>	12	HBV	env	28	A
IPQSLDRWWTSL	<u>2328</u>	12	HBV	env	28	A
IPQSLDSRWTS�	<u>2329</u>	12	HBV	env	28	A
IPQSLDSWWRSL	<u>2330</u>	12	HBV	env	28	A
IPQSLDSWWTRL	<u>2331</u>	12	HBV	env	28	A
YPQSLDSWWTSL	<u>2332</u>	12	HBV	env	28	A
IPYSLDSWWTSL	<u>2333</u>	12	HBV	env	28	A
IPQYLDSWWTSL	<u>2334</u>	12	HBV	env	28	A
IPQSLYSWWTSL	<u>2335</u>	12	HBV	env	28	A
IPQSLDYWWTSL	<u>2336</u>	12	HBV	env	28	A
IPQSLDSWYTSL	<u>2337</u>	12	HBV	env	28	A
IPQSLDSWWTYL	<u>2338</u>	12	HBV	env	28	A
IPGSLDSWWTSL	<u>2339</u>	12	HBV	env	28	A
IPQSLDSGWTSL	<u>2340</u>	12	HBV	env	28	A
IPQSLDSPWTSL	<u>2341</u>	12	HBV	env	28	A
IPQSLDSWGTSL	<u>2342</u>	12	HBV	env	28	A
IPQSLDSWPTSL	<u>2343</u>	12	HBV	env	28	A
IPQSLDSWWTGL	<u>2344</u>	12	HBV	env	28	A

MURINE CLASS I SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
IPQSLDSWWTPL	<u>2345</u>	12	HBV	env	28	A
IPQVLDSWWTSL	<u>2346</u>	12	HBV	env	28	A
IPQFLDSWWTSL	<u>2347</u>	12	HBV	env	28	A
IPQPLDSWWTSL	<u>2348</u>	12	HBV	env	28	A
IPQMLDSWWTSL	<u>2349</u>	12	HBV	env	28	A
IPQILDSWWTSL	<u>2350</u>	12	HBV	env	28	A
IPQLLDSWWTSL	<u>2351</u>	12	HBV	env	28	A
IPQGLDSWWTSL	<u>2352</u>	12	HBV	env	28	A
IPQTLDSWWTSL	<u>2353</u>	12	HBV	env	28	A
IPQHLDSWWTSL	<u>2354</u>	12	HBV	env	28	A
IPQCLDSWWTSL	<u>2355</u>	12	HBV	env	28	A
IPQNLDSWWTSL	<u>2356</u>	12	HBV	env	28	A
IPQQLDSWWTSL	<u>2357</u>	12	HBV	env	28	A
IPQWLDSWWTSL	<u>2358</u>	12	HBV	env	28	A
IPQDLDSWWTSL	<u>2359</u>	12	HBV	env	28	A
IPQKLDSWWTSL	<u>2360</u>	12	HBV	env	28	A
IPQSLVSWWTSL	<u>2361</u>	12	HBV	env	28	A
IPQSLFSWWTSL	<u>2362</u>	12	HBV	env	28	A
IPQSLPSWWTSL	<u>2363</u>	12	HBV	env	28	A
IPQSLMSWWTSL	<u>2364</u>	12	HBV	env	28	A
IPQSLISWWTSL	<u>2365</u>	12	HBV	env	28	A
IPQSLLSWWTSL	<u>2366</u>	12	HBV	env	28	A
IPQSLGSWWTSL	<u>2367</u>	12	HBV	env	28	A
IPQSLSSWWTSL	<u>2368</u>	12	HBV	env	28	A
IPQSLTSWWTSL	<u>2369</u>	12	HBV	env	28	A
IPQSLHSWWTSL	<u>2370</u>	12	HBV	env	28	A
IPQSLCSWWTSL	<u>2371</u>	12	HBV	env	28	A
IPQSLNSWWTSL	<u>2372</u>	12	HBV	env	28	A
IPQSLQSWWTSL	<u>2373</u>	12	HBV	env	28	A
IPQSLWSWWTSL	<u>2374</u>	12	HBV	env	28	A
IPQSLKSWWTSL	<u>2375</u>	12	HBV	env	28	A
IPSLDSWWTSL	<u>2376</u>	11	HBV	env	28	A
IPQSLDSWTSL	<u>2377</u>	11	HBV	env	28	A
IPQSLDSWWTL	<u>2378</u>	11	HBV	env	28	A
IPQALASWWTSL	<u>2379</u>	12	HBV	env	28	A
IPQSLDSWWTSM	<u>2380</u>	12	HBV	env	28	A
IPQSLDSWWTSF	<u>2381</u>	12	HBV	env	28	A
KTPSFPNI	<u>2382</u>	8	HBV	pol	75	
HAVEFHNL	<u>2383</u>	8	HBV	pol	289	
VSAAFYHL	<u>2384</u>	8	HBV	pol	419	
VIGCYGSL	<u>2385</u>	8	HBV	pol	588	
KQYLNLYPV	<u>2386</u>	9	HBV	pol	668	
CYGSLPQEH	<u>2387</u>	10	HBV	pol	591	
VSAAFYHL	<u>2388</u>	8	HBV	pol	419	
HAVEFHNL	<u>2389</u>	8	HBV	pol	289	
VIGCYGSL	<u>2390</u>	8	HBV	pol	588	
KTPSFPNI	<u>2391</u>	8	HBV	pol	75	
RPQSLDSWWTSL	<u>2392</u>	12	HBVs	env	28	A

MURINE CLASS I SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
IPQRLDSWWTSL	<u>2393</u>	12	HBVs	env	28	A
IPQSLRSWWTSL	<u>2394</u>	12	HBVs	env	28	A
IPQSLDRWWTSL	<u>2395</u>	12	HBVs	env	28	A
IPQSLDSRWTSLS	<u>2396</u>	12	HBVs	env	28	A
IPQSLDSWWRSLS	<u>2397</u>	12	HBVs	env	28	A
IPQSLDSWWTRL	<u>2398</u>	12	HBVs	env	28	A
IPQELDSWWTSL	<u>2399</u>	12	HBVs	env	28	A
IPQSLYSWWTSL	<u>2400</u>	12	HBVs	env	28	A
IPQSLDSWETSLS	<u>2401</u>	12	HBVs	env	28	A
IPQSLDSWWESLS	<u>2402</u>	12	HBVs	env	28	A
VESENKVV	<u>2403</u>	8	HCV	Entire	2253	
AGPYRAFVTI	<u>2404</u>	10	HIV	env	18	A
RAPYRAFVTI	<u>2405</u>	10	HIV	env	18	A
RGPYRAFVTA	<u>2406</u>	10	HIV	env	18	A
KGPYRAFVTI	<u>2407</u>	10	HIV	env	18	A
RGPYRAFVTK	<u>2408</u>	10	HIV	env	18	A
RGPGRAFVTI	<u>2409</u>	10	HIV	env	18	
RGPGRYFVTI	<u>2410</u>	10	HIV	env	18	A
RGPGRAYVTI	<u>2411</u>	10	HIV	env	18	A
RGPGRAFVTI	<u>2412</u>	10	HIV	env	18	A
VESMNKEL	<u>2413</u>	8	HIV	POL	903	
TDSQYALGI	<u>2414</u>	9	HIV	POL	689	
RGAYRAFVTI	<u>2415</u>	10	HIV		18	A
RGPARAFVTI	<u>2416</u>	10	HIV		18	A
RGPYRAAVTI	<u>2417</u>	10	HIV		18	A
RGPYRAFATI	<u>2418</u>	10	HIV		18	A
RGPYRAFVAI	<u>2419</u>	10	HIV		18	A
RGKYRAFVTI	<u>2420</u>	10	HIV		18	A
RGPFRAFVTI	<u>2421</u>	10	HIV		18	A
RGPYKAFVTI	<u>2422</u>	10	HIV		18	A
RGPYRKFTI	<u>2423</u>	10	HIV		18	A
RGPYRAYVTI	<u>2424</u>	10	HIV		18	A
RGPYRAFVTI	<u>2425</u>	10	HIV		18	A
RGPYRAFVKI	<u>2426</u>	10	HIV		18	A
NEILIRCI	<u>2427</u>	9	HPV	E6	97	
QEKKRHVDL	<u>2428</u>	9	HPV	E6	113	
LFVVYRDSI	<u>2429</u>	9	HPV	E6	52	
FYSRIRELRF	<u>2430</u>	10	HPV	E6	71	A
SSIEFARL	<u>2431</u>	8	HSV		498	
KVPRNQDWL	<u>2432</u>	9	Human	gp100		
VYDFYVWM	<u>2433</u>	8	Human	TRP2		A
KNKFFSYL	<u>2434</u>	8	Human	Tyrosinase	131	
LAVLYCLL	<u>2435</u>	8	Human	Tyrosinase	3	
YMVPFIPL	<u>2436</u>	8	Human	Tyrosinase	425	
GQMNGSTPM	<u>2437</u>	10	Human	Tyrosinase	157	
IVTMFEAL	<u>2438</u>	8	LCMV	GP	4	
ISHNFCNL	<u>2439</u>	8	LCMV	GP	118	
GVYQFKSV	<u>2440</u>	8	LCMV	GP	70	

MURINE CLASS I SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
HYISMGTSGL	<u>2441</u>	10	LCMV	GP	99	
SGVENPGGYCL	<u>2442</u>	11	LCMV	GP	276	
KAVYNFATM	<u>2443</u>	9	LCMV	GP	33	
CMANNSHHYI	<u>2444</u>	10	LCMV	GP	92	A
CSANNSHHYM	<u>2445</u>	10	LCMV	GP	92	A
SMVENPGGYCL	<u>2446</u>	11	LCMV	GP	276	A
SGVENPGGYCM	<u>2447</u>	11	LCMV	GP	276	A
KAVYNFATM	<u>2448</u>	9	LCMV	GP	33	
KAVYNAATM	<u>2449</u>	9	LCMV	GP	33	A
KAVANFATM	<u>2450</u>	9	LCMV	GP	33	A
KAVYNYATM	<u>2451</u>	9	LCMV	GP	33	A
KAVYNFAAM	<u>2452</u>	9	LCMV	GP	33	A
YTVKYPNL	<u>2453</u>	8	LCMV	NP	205	
FQPQNGQFI	<u>2454</u>	9	LCMV	NP	396	
VGLSYSQTM	<u>2455</u>	9	LCMV	NP	356	
FQPQNGQFI	<u>2456</u>	9	LCMV	NP	396	
FQPQNGQFIHFY	<u>2457</u>	12	LCMV	NP	396	
RPQASGVYM	<u>2458</u>	9	LCMV	NP	118	
RPQASQVYM	<u>2459</u>	9	LCMV	NP	118	A
YTYKYPNL	<u>2460</u>	8	LCMV	NP	205	A
RPQASGVYM	<u>2461</u>	9	LCMV	NP	118	A
RPQASGVAM	<u>2462</u>	9	LCMV	NP	118	A
RPQGSQVYM	<u>2463</u>	9	LCMV	NP	118	A
RPNASGVYM	<u>2464</u>	9	LCMV	NP	118	A
KAVYNFATCGI	<u>2465</u>	11	LCMV			
KAVYNFATB	<u>2466</u>	9	LCMV			
VYAKECTGL	<u>2467</u>	9	Lysteria	listeriolysin	479	
YPHFMPTNL	<u>2468</u>	9	MCMV		168	
YPHYMPTNL	<u>2469</u>	9	MCMV		168	A
HETTYNSI	<u>2470</u>	8	Mouse	beta actin	275	A
YEDTGKTI	<u>2471</u>	8	Mouse	p40 phox RNA	245	
LGYDYSYL	<u>2472</u>	8	Mouse	Tyrosinase	445	
SSMHNALHI	<u>2473</u>	9	Mouse	Tyrosinase	360	
ANFSFRNTL	<u>2474</u>	9	Mouse	Tyrosinase	336	
SYLTLAKHT	<u>2475</u>	9	Mouse	Tyrosinase	136	
HYYVSRDTL	<u>2476</u>	9	Mouse	Tyrosinase	180	
YYVSRDTLL	<u>2477</u>	9	Mouse	Tyrosinase	181	
SFFSSWQII	<u>2478</u>	9	Mouse	Tyrosinase	267	
SYMVPFIPL	<u>2479</u>	9	Mouse	Tyrosinase	424	
PYLEQASRI	<u>2480</u>	9	Mouse	Tyrosinase	466	
SYLTLAKHTI	<u>2481</u>	10	Mouse	Tyrosinase	136	
HYYVSRDTLL	<u>2482</u>	10	Mouse	Tyrosinase	180	
SQVMNLHNL	<u>2483</u>	9	Mouse	TYRP2	363	
YENDIEKKI	<u>2484</u>	9	P. falciparum	CSP	375	
NEEPSDKHI	<u>2485</u>	9	P. falciparum	CSPZ	347	
EEKHEKKHV	<u>2486</u>	9	P. falciparum	LSA1	52	
SYVPSAEQIL	<u>2487</u>	10	P. yoelii	CSP	280	
RYLENGKETL	<u>2488</u>	10	Unknown	HLA-A24	170	

MURINE CLASS I SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
RYLKNGKETL	<u>2489</u>	10	Unknown	HLA-Cw3	170	
IYTQNRRL	<u>2490</u>	9	Unknown	P815	12	
VYDFFVWM	<u>2491</u>	8	Unknown	TRP2	181	A
SVYDFFVWL	<u>2492</u>	9	Unknown	TRP2	180	
SVYDFYVWM	<u>2493</u>	9	Unknown	TRP2	180	A
ASNENMDAM	<u>2494</u>	9	unknown			
FAPGYNPAL	<u>2495</u>	9	unknown			
SIQFFGERAL	<u>2496</u>	10	unknown			
SIQFFGEL	<u>2497</u>	8	unknown			
RGYVYQGL	<u>2498</u>	8	VSV	NP	52	
RGPRNLNTL	<u>2499</u>	8				
HMWNFIGV	<u>2500</u>	8				
GGAYRLIVF	<u>2501</u>	9				
KYLVTRHADV	<u>2502</u>	19				
FSPRRNGYL	<u>2503</u>	9				
SHYAFSPM	<u>2177</u>	8				
FQPQNGQFI	<u>2290</u>	9				

TABLE 29

MURINE CLASS I SUPERTYPE							
Sequence	SEQ ID NO.	Dd	Kb	Kd	Db	Ld	Kk
SGPSNTPPEI	<u>2202</u>	18500	>31000	>10000	8.1		
RNPRFYNL	<u>2203</u>		7.9		>44000		
QPQRGYENF	<u>2204</u>					319	
SEAAAYAKKI	<u>2205</u>						3.9
AYAPAKAAI	<u>2206</u>			3.5			
AYAEAKAAI	<u>2207</u>			50			
AYANAKAAI	<u>2208</u>			60			
AYAGAKAAI	<u>2209</u>			48			
AYAVAKAAI	<u>2210</u>			42			
AAAAYAAM	<u>2211</u>		375		>44000		
AAAAYAAAAM	<u>2212</u>		228		>44000		
AAAANAAAM	<u>2213</u>		10960		23		
AAAAAANAAA	<u>2214</u>		31000		257		
M	<u>2215</u>		484				
NAIVFKGL	<u>2216</u>		3.7				
SIINFEKL	<u>2217</u>		195				
IFYCPIAI	<u>2218</u>		92				
KVVRFDKL	<u>2219</u>			303			
VYSFSLASRL	<u>2220</u>	>37000	1.5	>10000	30508		
SIINFEKL	<u>2221</u>		37				
KVVRFDKL	<u>2222</u>						13
SENDRYRL	<u>2223</u>			>10000	304		
SFYRNLLWL	<u>2224</u>						0.65
YEANGNLI	<u>2225</u>		16				
MGLIYNRM	<u>2226</u>		2.3				
MGYIYNRM	<u>2227</u>		14				
MGLIFNRM	<u>2228</u>		21				
MGLIYNRM	<u>2229</u>		9.9				
RMIQNSLTI	<u>2230</u>				4.6		
RLIQNFLTI	<u>2231</u>				40		
GMRQNATEI	<u>2232</u>				81		
YMRVNGKWM	<u>2233</u>				50		
FYIQMATEL	<u>2234</u>			0.31			
FYIQMCTFL	<u>2235</u>			1.1			
AYERMANIL	<u>2236</u>			233			
AYQRM CNIL	<u>2237</u>			2.7			
AYERMCTIL	<u>2238</u>			4.1			
ASNENMETM	<u>2239</u>	>37000	>31000	>10000	33		
TYQRTRALM	<u>2240</u>			69			
TYQKTRALV	<u>2241</u>			44			
TYQPTRALV	<u>2242</u>			17			
TYQFTRALV	<u>2243</u>			371			
TYQLTRALV	<u>2244</u>			110			
SDYEGRLI	<u>2245</u>						0.60
MITQFESL	<u>2246</u>		64				
RTFSFQLI	<u>2247</u>		26				

MURINE CLASS I SUPERTYPE							
Sequence	SEQ ID NO.	Dd	Kb	Kd	Db	Ld	Kk
FSVIFDRL	<u>2248</u>		201				
RTFSFQLI	<u>2249</u>		27				
MITQFESL	<u>2250</u>		42				
FSVIFDRL	<u>2251</u>		115				
KSSFYRNL	<u>2252</u>		209				
SSLPFQNI	<u>2253</u>		53				
MNIQFTAV	<u>2254</u>		131				
MNYYWTLL	<u>2255</u>		169				
SFYRNLLWL	<u>2256</u>				46		
SSLPFQNI	<u>2257</u>		9.5				
MNIQFTAV	<u>2258</u>		26				
MNYYWTLL	<u>2259</u>		56				
KSSFYRNL	<u>2260</u>		117				
SIIPSGPL	<u>2261</u>		393				
LSYSAGAL	<u>2262</u>		60				
LSYSAGAL	<u>2263</u>		31				
SSISFCGV	<u>2264</u>		29				
TGICNQNI	<u>2265</u>				13		
ITYKNSTWV	<u>2266</u>				409		
FCGVNSDTV	<u>2267</u>				206		
TGICNQNI	<u>2268</u>				21		
FCGVNSDTV	<u>2269</u>				166		
ITYKNSTWV	<u>2270</u>				276		
SSISFCGV	<u>2271</u>		2.3				
IGRFYIQM	<u>2272</u>		42				
MMIWHSNL	<u>2273</u>		238				
ASNENMETM	<u>2274</u>				41		
IGRFYIQM	<u>2275</u>		24				
MMIWHSNL	<u>2276</u>		287				
FFYRYGFV	<u>2277</u>		350				
KMITQRTI	<u>2278</u>		300				
RSYLIRAL	<u>2279</u>		103				
RFYRTCKL	<u>2280</u>		117				
TALANTIEV	<u>2281</u>				16		
TALANTIEV	<u>2282</u>				3.7		
RSYLIRAL	<u>2283</u>		78				
RFYRTCKL	<u>2284</u>		47				
VYINTALL	<u>2285</u>		65				
VYINTALL	<u>2286</u>		14				
VYIEVLHL	<u>2287</u>		75				
VYIEVLHL	<u>2288</u>		21				
WYIPPSLRTL	<u>2289</u>			96			
MURTAZAKDPE				0.96			
PTIDES							
IYSTVASSL	<u>2291</u>			4.1			
LYEKVKSQL	<u>2292</u>			2.2			
LYQVKSQL	<u>2293</u>			2.8			
LYEKMKSQL	<u>2294</u>			1.6			

MURINE CLASS I SUPERTYPE							
Sequence	SEQ ID NO.	Dd	Kb	Kd	Db	Ld	Kk
LYEKVFSQL	<u>2295</u>			7.4			
LYQNVGTYV	<u>2296</u>			6.9			
MGLKFRQL	<u>2297</u>		7.4				
VSyvNTNM	<u>2298</u>		60				
SYVNTNMGL	<u>2299</u>			19			
MGLKFRQL	<u>2300</u>		6.3				
VSyvNTNM	<u>2301</u>		33				
SYVNTNMGL	<u>2302</u>			12			
WGPSLYSI	<u>2303</u>	17					
ASARFSWL	<u>2304</u>		323				
WGPSLYSIL	<u>2305</u>	6.6					
TGPCRTCMT	<u>2306</u>	108					
WYWGPSLYSI	<u>2307</u>			8.3			
IPQSLDSWWTS L	<u>2308</u>					2.2	
IPQSLDSYWTS�	<u>2309</u>					2.7	
ASARFSWL	<u>2310</u>		49				
WYWGPSLYSI	<u>2311</u>			16			
APQSLDSWWTS L	<u>2312</u>					15	
IPQALDSWWTS L	<u>2313</u>					6.1	
IPQSLASWWTS L	<u>2314</u>					4.2	
IPQSLDAWWTS L	<u>2315</u>					4.0	
IPQSLDSAWTS�	<u>2316</u>					13	
IPQSLDSWWAS L	<u>2317</u>					0.34	
IPQSLDSWWTA L	<u>2318</u>					134	
EPQSLDSWWTS L	<u>2319</u>					86	
IPESLDSWWTS�	<u>2320</u>					13	
IPQSLDEWWTS L	<u>2321</u>					1.9	
IPQSLDSWWTE L	<u>2322</u>					3.0	
RPQSLDSWWTS L	<u>2323</u>					60	
IPRSLDSWWTS L	<u>2324</u>					160	
IPQRLDSWWTS L	<u>2325</u>					23	
IPQSRDSWWTS L	<u>2326</u>					21	
IPQSLRWWTS L	<u>2327</u>					12	
IPQSLDRWWTS L	<u>2328</u>					5.0	
IPQSLDSRWTS�	<u>2329</u>					47	
IPQSLDSWWRS L	<u>2330</u>					485	
IPQSLDSWWTR L	<u>2331</u>					196	
YPQSLDSWWTS L	<u>2332</u>					91	

MURINE CLASS I SUPERTYPE							
Sequence	SEQ ID NO.	Dd	Kb	Kd	Db	Ld	Kk
IPYSLDSWWTS						0.78	
L	<u>2333</u>						
IPQYLDSWWTS						92	
L	<u>2334</u>						
IPQSLYSWWTS						4.7	
L	<u>2335</u>						
IPQSLDYWWTS						1.6	
L	<u>2336</u>						
IPQSLDSWYTSL	<u>2337</u>					17	
IPQSLDSWWTY						0.89	
L	<u>2338</u>						
IPGSLDSWWTS						24	
L	<u>2339</u>						
IPQSLDSGWTS	<u>2340</u>					70	
IPQSLDSPWTS	<u>2341</u>					19	
IPQSLDSWGTSL	<u>2342</u>					138	
IPQSLDSWPTSL	<u>2343</u>					60	
IPQSLDSWWTG						2.5	
L	<u>2344</u>						
IPQSLDSWWTP						1.2	
L	<u>2345</u>						
IPQVLDSWWTS						5.1	
L	<u>2346</u>						
IPQFLDSWWTS						4.3	
L	<u>2347</u>						
IPQPLDSWWTS						6.3	
L	<u>2348</u>						
IPQMLDSWWTS						4.1	
L	<u>2349</u>						
IPQILDSWWTS	<u>2350</u>					12	
IPQLLDSWWTS						0.25	
L	<u>2351</u>						
IPQGLDSWWTS						2.7	
L	<u>2352</u>						
IPQTLDSWWTS						7.7	
L	<u>2353</u>						
IPQHLDSWWTS						39	
L	<u>2354</u>						
IPQCLDSWWTS						25	
L	<u>2355</u>						
IPQNLDSWWTS						12	
L	<u>2356</u>						
IPQQLDSWWTS						1.7	
L	<u>2357</u>						
IPQWLDSWWTS						3.7	
L	<u>2358</u>						
IPQDLDSWWTS						22	
L	<u>2359</u>						
IPQKLDWWTS						9.3	
L	<u>2360</u>						
IPQSLVSWWTS						11	
L	<u>2361</u>						
IPQSLFSWWTS	<u>2362</u>					11	
IPQSLPSWWTS	<u>2363</u>					16	
IPQSLMSWWTS						0.95	
L	<u>2364</u>						
IPQSLISWWTS	<u>2365</u>					17	
IPQSLLSWWTS	<u>2366</u>					0.84	
IPQSLGWWTS	<u>2367</u>					2.7	

MURINE CLASS I SUPERTYPE							
Sequence	SEQ ID NO.	Dd	Kb	Kd	Db	Ld	Kk
L							
IPQSLSSWWTSL	<u>2368</u>					0.49	
IPQSLTSWWTSL	<u>2369</u>					1.7	
IPQSLHSWWTS						1.5	
L	<u>2370</u>						
IPQSLCSWWTS						1.1	
L	<u>2371</u>						
IPQSLNSWWTS						1.5	
L	<u>2372</u>						
IPQSLQSWWTS						0.81	
L	<u>2373</u>						
IPQSLWSWWTS						2.4	
L	<u>2374</u>						
IPQSLKSWWTS						1.1	
L	<u>2375</u>						
IPSLDSWWTSL	<u>2376</u>					119	
IPQSLDSWTSL	<u>2377</u>					0.22	
IPQSLDSWWTL	<u>2378</u>					1.3	
IPQALASWWTS						26	
L	<u>2379</u>						
IPQSLDSWWTS						0.80	
M	<u>2380</u>						
IPQSLDSWWTS						1.9	
F	<u>2381</u>						
KTPSFPNI	<u>2382</u>		270				
HAVEFHNL	<u>2383</u>		49				
VSAAFYHL	<u>2384</u>		7.0				
VIGCYGSL	<u>2385</u>		157				
KQYLNLYPV	<u>2386</u>				3.4		
CYGSLPQEH	<u>2387</u>			303			
VSAAFYHL	<u>2388</u>		5.2				
HAVEFHNL	<u>2389</u>		158				
VIGCYGSL	<u>2390</u>		63				
KTPSFPNI	<u>2391</u>		155				
RPQSLDSWWTS						144	
L	<u>2392</u>						
IPQRLDSWWTS						34	
L	<u>2393</u>						
IPQSLRSWWTS						11	
L	<u>2394</u>						
IPQSLDRWWTS						2.0	
L	<u>2395</u>						
IPQSLDSRWTS	<u>2396</u>					2.6	
IPQSLDSWWRS						335	
L	<u>2397</u>						
IPQSLDSWWTR						27	
L	<u>2398</u>						
IPQELDSWWTS						18	
L	<u>2399</u>						
IPQSLYSWWTS						8.3	
L	<u>2400</u>						
IPQSLDSWETSL	<u>2401</u>					5.3	
IPQSLDSWWES						394	
L	<u>2402</u>						
VESENKVV	<u>2403</u>						349
AGPYRAFVTI	<u>2404</u>	5.0					

MURINE CLASS I SUPERTYPE							
Sequence	SEQ ID NO.	Dd	Kb	Kd	Db	Ld	Kk
RAPYRAFVTI	<u>2405</u>	176					
RGPYRAFVTA	<u>2406</u>	126					
KGPYRAFVTI	<u>2407</u>	5.8					
RGPYRAFVTK	<u>2408</u>	91					
RGPGRAFVTI	<u>2409</u>	9.7	31000	>10000	22000		
RGPGRYFVTI	<u>2410</u>	2.7					
RGPGRAYVTI	<u>2411</u>	14					
RGPGRAFVTI	<u>2412</u>	7.2					
VESMNKEL	<u>2413</u>						114
TDSQYALGI	<u>2414</u>						179
RGAYRAFVTI	<u>2415</u>	3.4					
RGPARAFVTI	<u>2416</u>	1.04					
RGPYRAAVTI	<u>2417</u>	2.0					
RGPYRAFATI	<u>2418</u>	2.1					
RGPYRAFVAI	<u>2419</u>	1.3					
RGKYRAFVTI	<u>2420</u>	67					
RGPFRAFVTI	<u>2421</u>	0.78					
RGPYKAFVTI	<u>2422</u>	13					
RGPYRKFTI	<u>2423</u>	3.6					
RGPYRAYVTI	<u>2424</u>	2.1					
RGPYRAFVTI	<u>2425</u>	2.3					
RGPYRAFVKI	<u>2426</u>	3.9					
NEILIRCI	<u>2427</u>						12
QEKKRHVDL	<u>2428</u>						256
LFVVYRDSI	<u>2429</u>			453			
FYSRIRELRF	<u>2430</u>			447			
SSIEFARL	<u>2431</u>		1.8	>10000			
KVPRNQDWL	<u>2432</u>				38		
VYDFYVWM	<u>2433</u>		145				
KNKFYSYL	<u>2434</u>		57				
LAVLYCLL	<u>2435</u>		72				
YMPVFIPL	<u>2436</u>		70				
GQMNGSTPM	<u>2437</u>				242		
IVTMFEAL	<u>2438</u>		82				
ISHNFCNL	<u>2439</u>		411				
GVYQFKSV	<u>2440</u>		11				
HYISMGTSGL	<u>2441</u>			83			
SGVENPGGYCL	<u>2442</u>		>31000		60		
KAVYNFATM	<u>2443</u>				3.3		
CMANNSHHYI	<u>2444</u>				220		
CSANNSHHYM	<u>2445</u>				42		
SMVENPGGYCL	<u>2446</u>				154		
SGVENPGGYCM	<u>2447</u>				128		
KAVYNFATM	<u>2448</u>				1.5	>27000	
KAVYNAATM	<u>2449</u>				2.0	>27000	
KAVANFATM	<u>2450</u>				1.2	27000	
KAVYNYATM	<u>2451</u>				2.1	>27000	
KAVYNFAAM	<u>2452</u>				4.4	27000	


MURINE CLASS I SUPERTYPE							
Sequence	SEQ ID NO.	Dd	Kb	Kd	Db	Ld	Kk
YTVKYPNL	<u>2453</u>		204				
FQPQNGQFI	<u>2454</u>				6.9		
VGLSYSQTM	<u>2455</u>		71				
FQPQNGQFI	<u>2456</u>		>31000		4.9		
FQPQNGQFIHFY	<u>2457</u>		15500		280		
RPQASGVYM	<u>2458</u>		>31000		>44000	0.99	
RPQASQVYM	<u>2459</u>					3.8	
YTYKYPNL	<u>2460</u>		1.8				
RPQASGVYM	<u>2461</u>					3.0	
RPQASGVAM	<u>2462</u>					12	
RPQSGGVYM	<u>2463</u>					39	
RPNASGVYM	<u>2464</u>					19	
KAVYNFATCGI	<u>2465</u>				29		
KAVYNFATB	<u>2466</u>				7.9		
VYAKECTGL	<u>2467</u>			129			
YPHFMPNTL	<u>2468</u>					7.5	
YPHYMPTNL	<u>2469</u>					9.5	
HETTYNSI	<u>2470</u>						1.8
YEDTGKTI	<u>2471</u>						0.86
LGYDYSYL	<u>2472</u>		3.4				
SSMHNALHI	<u>2473</u>				7.6		
ANFSFRNTL	<u>2474</u>		6.0				
SYLTLAKHT	<u>2475</u>			188			
HYYVSRDTL	<u>2476</u>			43			
YYVSRDTLL	<u>2477</u>			99			
SFFSSWQII	<u>2478</u>			16			
SYMVPFIPL	<u>2479</u>			144			
PYLEQASRI	<u>2480</u>			173			
SYLTLAKHTI	<u>2481</u>			4.4			
HYYVSRDTLL	<u>2482</u>			167			
SQVMNLHNL	<u>2483</u>				2.3		
YENDIEKKI	<u>2484</u>						3.8
NEEPSDKHI	<u>2485</u>						40
EEKHEKKHV	<u>2486</u>						284
SYVPSAEQIL	<u>2487</u>			280			
RYLENGKETL	<u>2488</u>			80			
RYLKNGKETL	<u>2489</u>			217			
IYTQNRRL	<u>2490</u>			144			
VYDFFVWM	<u>2491</u>		464				
SVYDFFVWL	<u>2492</u>		1.0				
SVYDFYVWM	<u>2493</u>		1.2		3365		
ASNENMDAM	<u>2494</u>				28		
FAPGYNPAL	<u>2495</u>		2.0				
SIQFFGERAL	<u>2496</u>		21		>44000		
SIQFFGEL	<u>2497</u>		16		>44000		
RGYVYQGL	<u>2498</u>	>37000	2.1	>10000	>44000		
RGPRLNTL	<u>2499</u>	186					
HMWNFIGV	<u>2500</u>		202				

MURINE CLASS I SUPERTYPE							
Sequence	<u>SEQ ID NO.</u>	Dd	Kb	Kd	Db	Ld	Kk
GGAYRLIVF	<u>2501</u>	3.5					
KYLVTRHADV	<u>2502</u>			33			
FSPRRNGYL	<u>2503</u>	2.7					
SHYAFSPM	<u>2177</u>		250		>88000		
FQPQNGQFI	<u>2290</u>		9513		17		


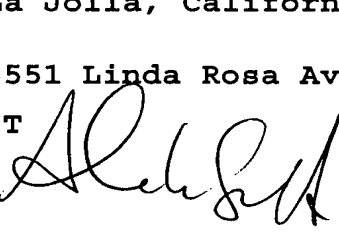
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VIII-4-1	Declaration: Inventorship (only for the purposes of the designation of the United States of America) Declaration of inventorship (Rules 4.17(iv) and 51bis.1(a)(iv)) for the purposes of the designation of the United States of America:	<p>I hereby declare that I believe I am the original, first and sole (if only one inventor is listed below) or joint (if more than one inventor is listed below) inventor of the subject matter which is claimed and for which a patent is sought.</p> <p>This declaration is directed to the international application of which it forms a part (if filing declaration with application).</p> <p>I hereby declare that my residence, mailing address, and citizenship are as stated next to my name.</p> <p>I hereby state that I have reviewed and understand the contents of the above-identified international application, including the claims of said application. I have identified in the request of said application, in compliance with PCT Rule 4.10, any claim to foreign priority, and I have identified below, under the heading "Prior Applications," by application number, country or Member of the World Trade Organization, day, month and year of filing, any application for a patent or inventor's certificate filed in a country other than the United States of America, including any PCT international application designating at least one country other than the United States of America, having a filing date before that of the application on which foreign priority is claimed.</p>
VIII-4-1 -1	Prior applications:	60/416,207, US, 03 October 2002 (03.10.2002) 60/417,269, US, 08 October 2002 (08.10.2002)

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		<p>I hereby acknowledge the duty to disclose information that is known by me to be material to patentability as defined by 37 C.F.R. § 1.56, including for continuation-in-part applications, material information which became available between the filing date of the prior application and the PCT international filing date of the continuation-in-part application.</p> <p>I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.</p>
VIII-4-1 -1-1	Name:	SIDNEY, John
VIII-4-1 -1-2	Residence: (city and either US State, if applicable, or country)	San Diego, California
VIII-4-1 -1-3	Mailing address:	4218 Corte de la Siena
VIII-4-1 -1-4	Citizenship:	US
VIII-4-1 -1-5	Inventor's Signature: (if not contained in the request, or if declaration is corrected or added under Rule 26ter after the filing of the international application. The signature must be that of the inventor, not that of the agent)	
VIII-4-1 -1-6	Date: (of signature which is not contained in the request, or of the declaration that is corrected or added under Rule 26ter after the filing of the international application)	11/17/03

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VIII-4-1 -2-1	Name:	SOUTHWOOD, Scott
VIII-4-1 -2-2	Residence: (city and either US State, if applicable, or country)	Santee, California
VIII-4-1 -2-3	Mailing address:	10679 Strathmore Drive
VIII-4-1 -2-4	Citizenship:	US
VIII-4-1 -2-5	Inventor's Signature: (If not contained in the request, or if declaration is corrected or added under Rule 26ter after the filing of the international application. The signature must be that of the inventor, not that of the agent)	
VIII-4-1 -2-6	Date: (of signature which is not contained in the request, or of the declaration that is corrected or added under Rule 26ter after the filing of the international application)	11/5/03
VIII-4-1 -3-1	Name:	SETTE, Alessandro
VIII-4-1 -3-2	Residence: (city and either US State, if applicable, or country)	La Jolla, California
VIII-4-1 -3-3	Mailing address:	5551 Linda Rosa Avenue
VIII-4-1 -3-4	Citizenship:	IT
VIII-4-1 -3-5	Inventor's Signature: (if not contained in the request, or if declaration is corrected or added under Rule 26ter after the filing of the international application. The signature must be that of the inventor, not that of the agent)	
VIII-4-1 -3-6	Date: (of signature which is not contained in the request, or of the declaration that is corrected or added under Rule 26ter after the filing of the international application)	11/17/03